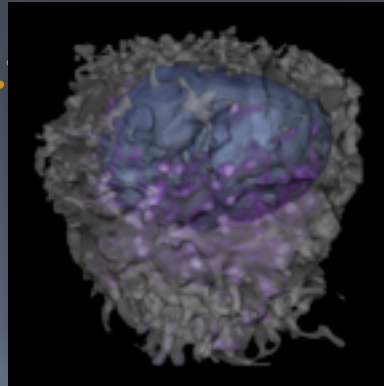


3-D views of nuclear organization and chromatin topology with x-ray tomography

Carolyn Larabell

University of California, San Francisco
Lawrence Berkeley National Laboratory



Bend magnet source

Branchline

End station

National Center for X-ray Tomography

ncxt.lbl.gov

NIH-NIGMS
NIH Epigenomics Roadmap Grant
NIH-NIDA

DOE-Biological and Environmental Research
Gordon and Betty Moore Foundation

Why soft x-ray tomography?

- Image biological specimens up to $15\mu\text{m}$ thick
- Specimens in near-native state
 - Hydrated
 - Cryo-immobilized
- High-contrast images without dyes or stains
- Quantitative
- Better than 50 nm resolution (isotropic)
- Localize molecules with respect to cell structures
 - Correlated fluorescence and x-ray tomography

Lawrence Berkeley National Laboratory

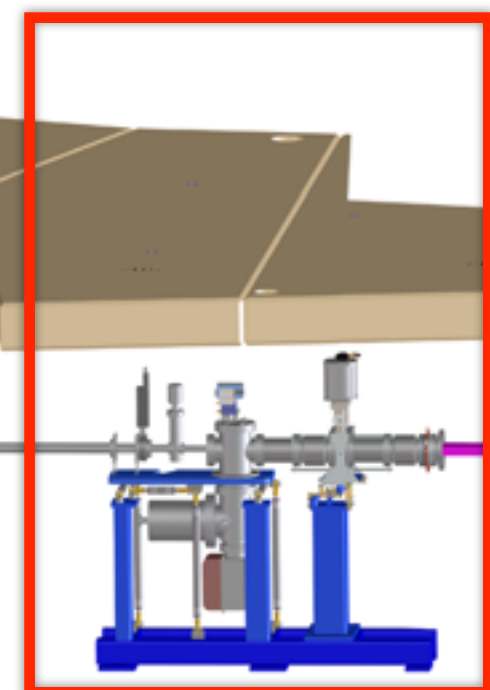


Full-field transmission x-ray microscope

Whole, hydrated, unfixed, unstained cells
50 nm isotropic resolution



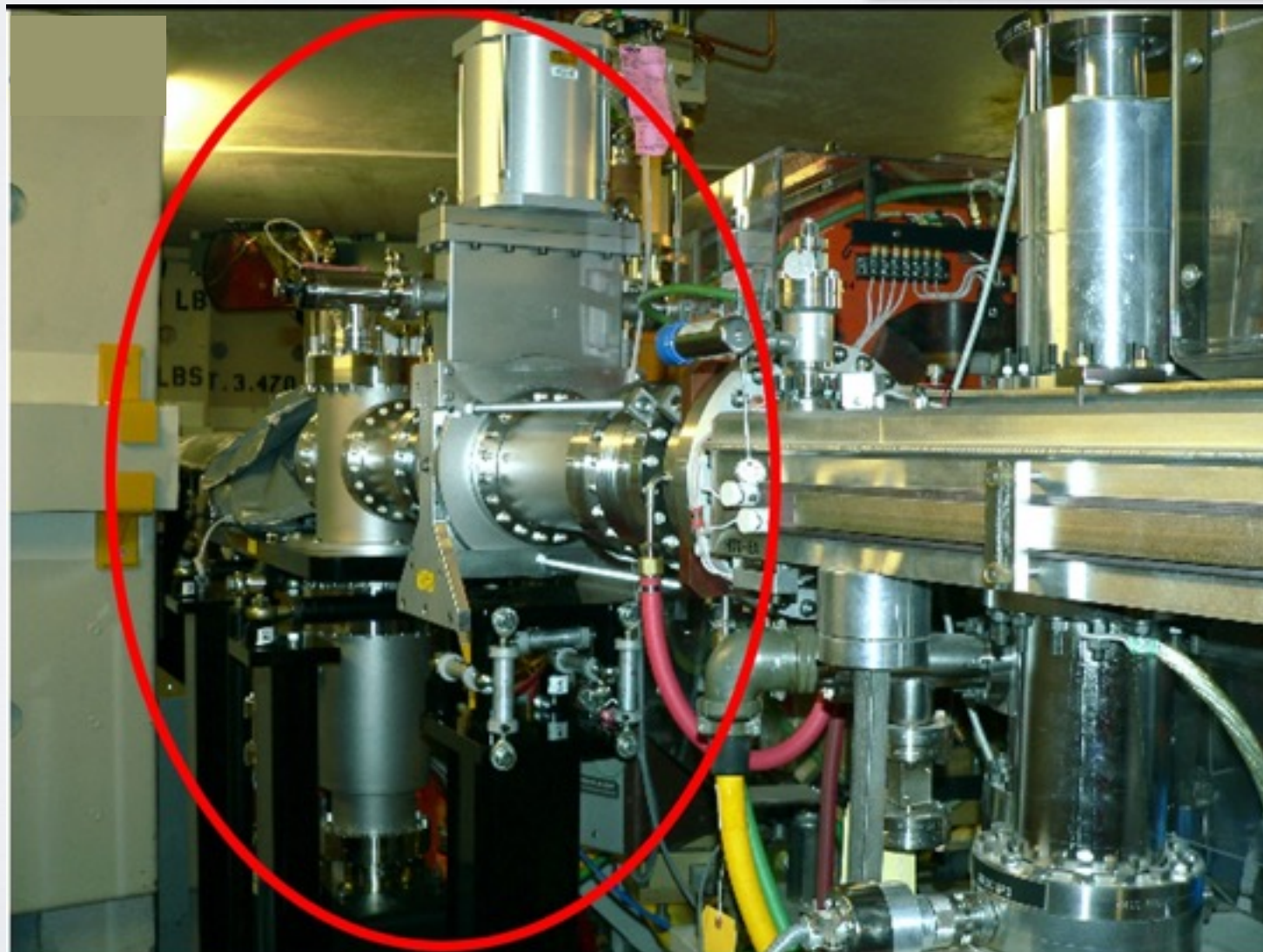
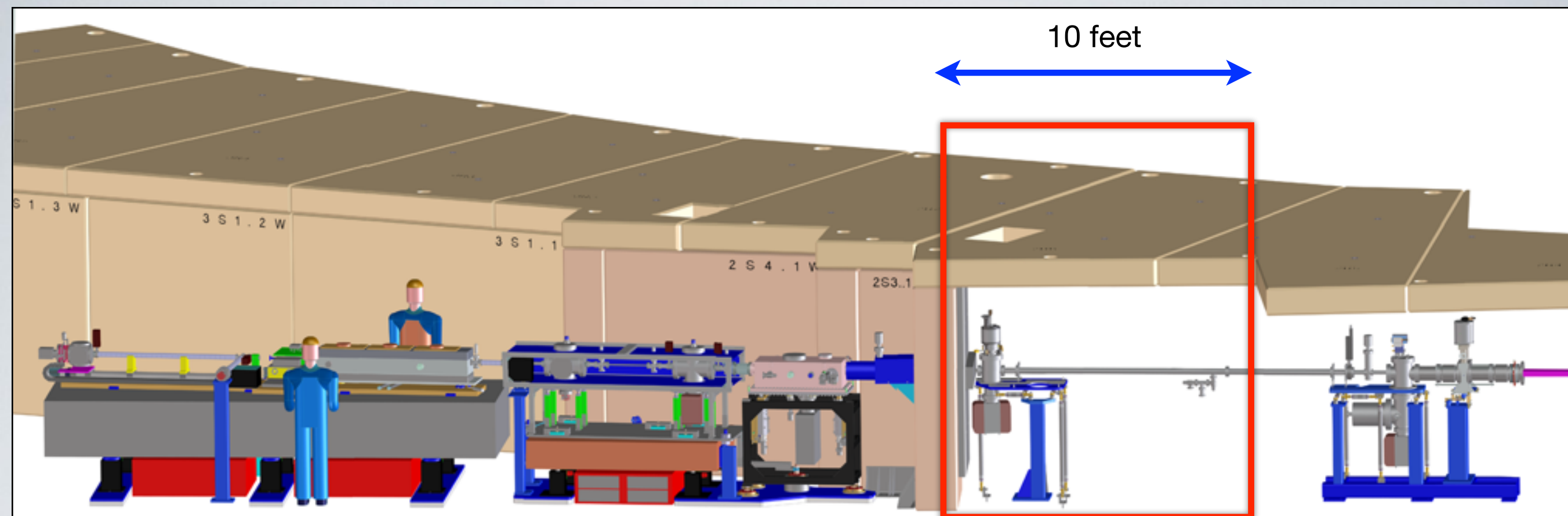
10 feet



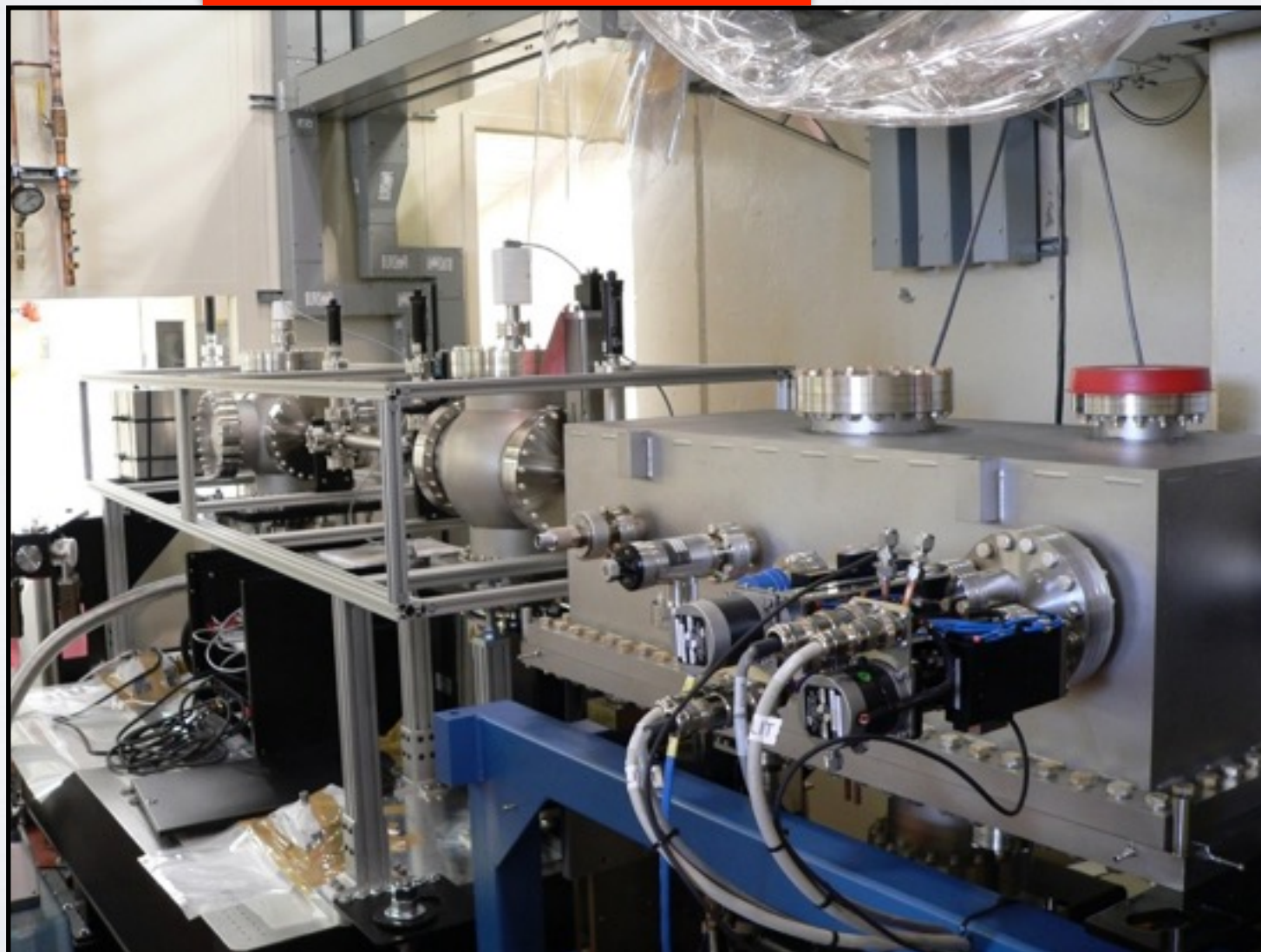
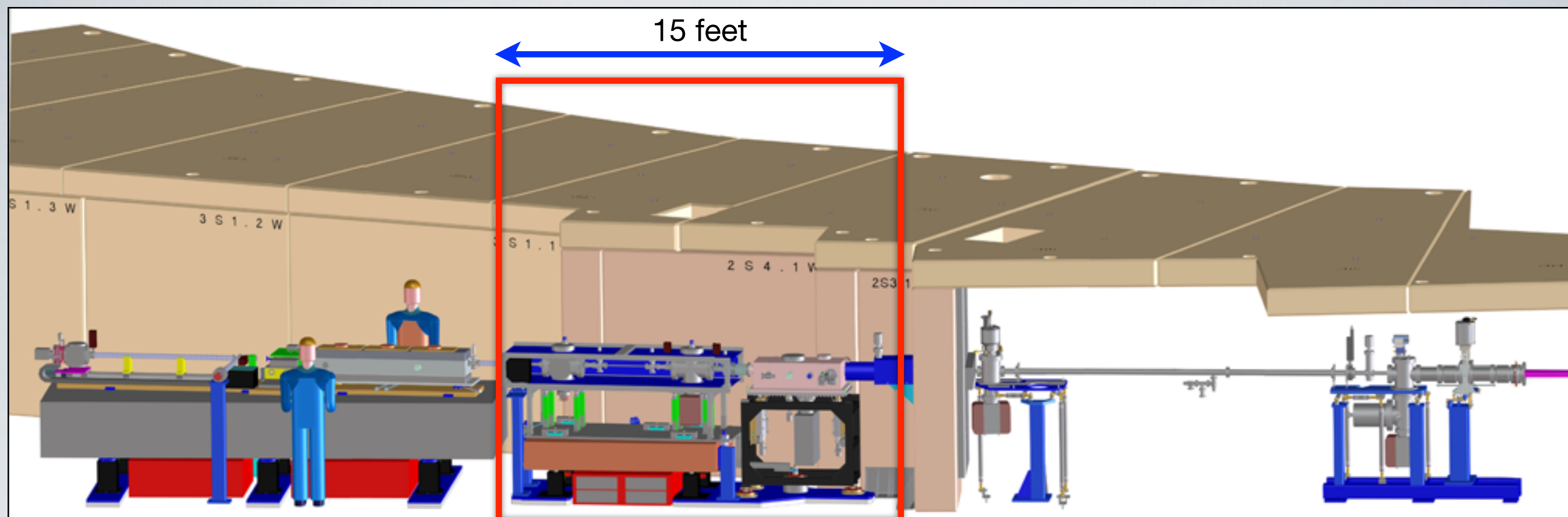
photon
shutter



10 feet

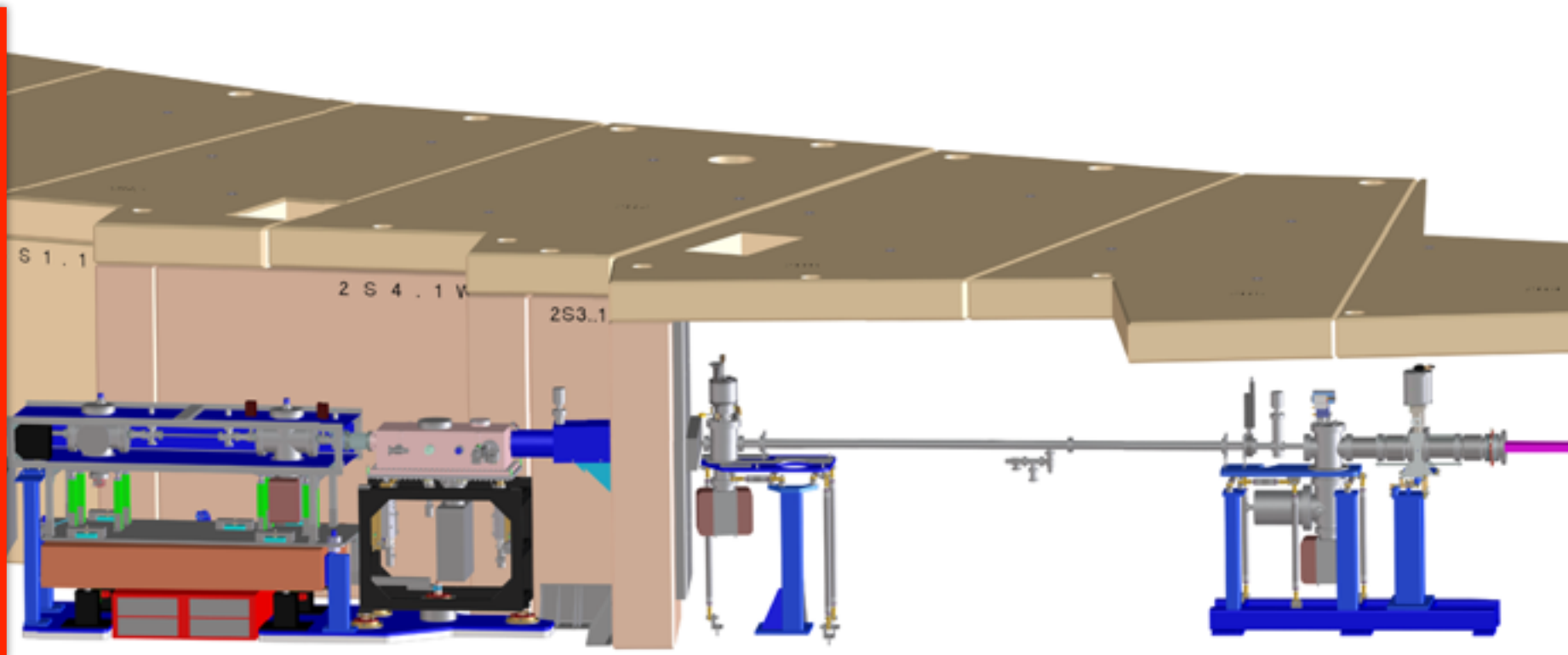
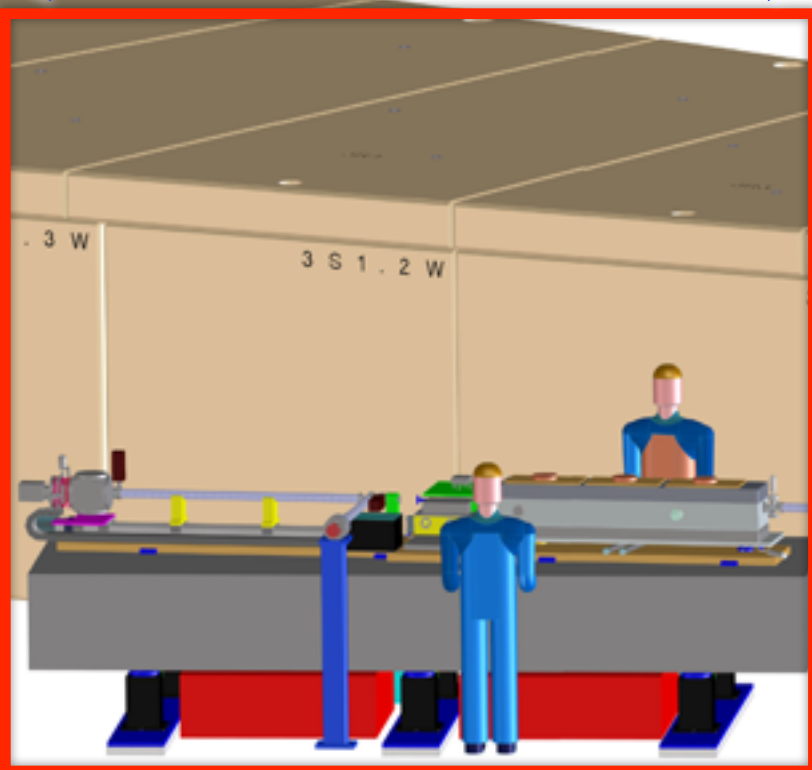


personnel
safety shutter



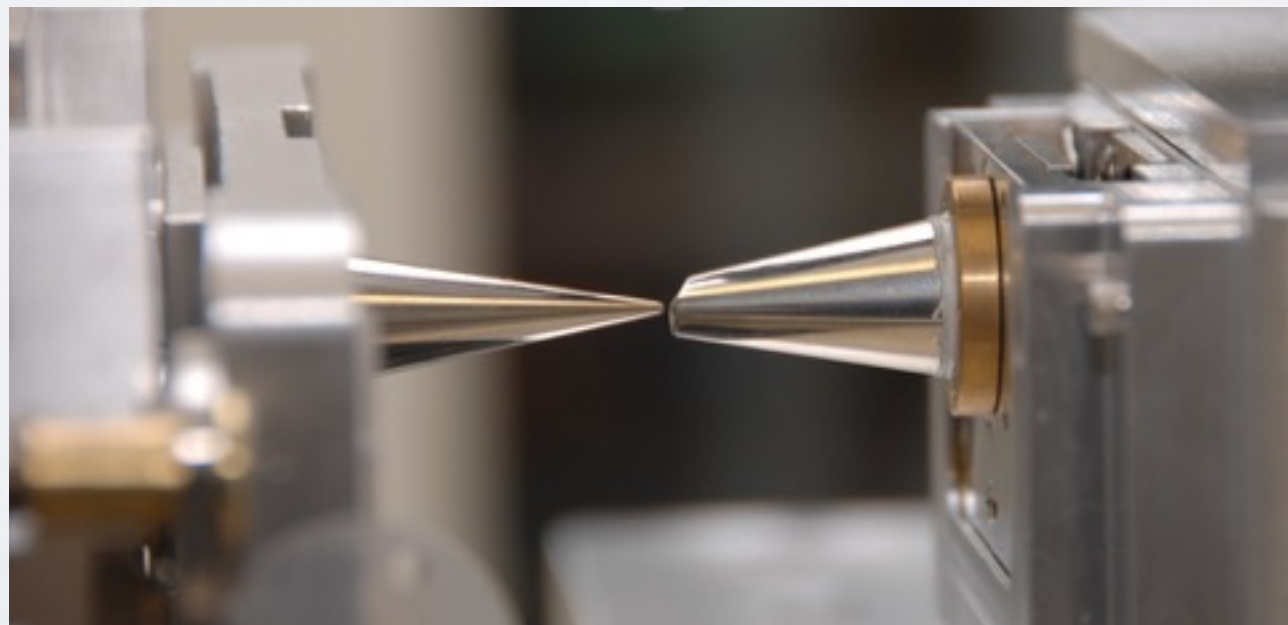
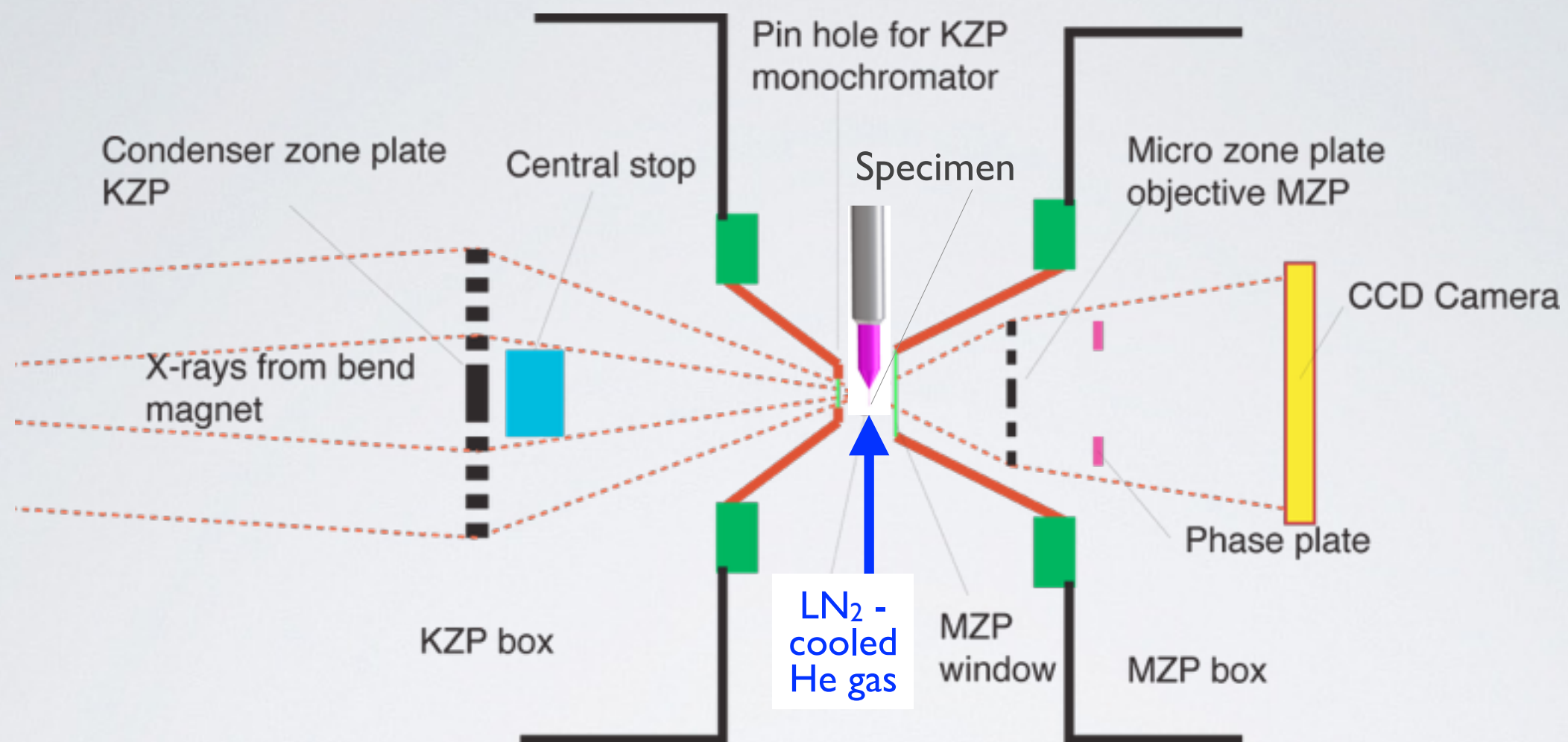
mirror and
branchline

15 feet

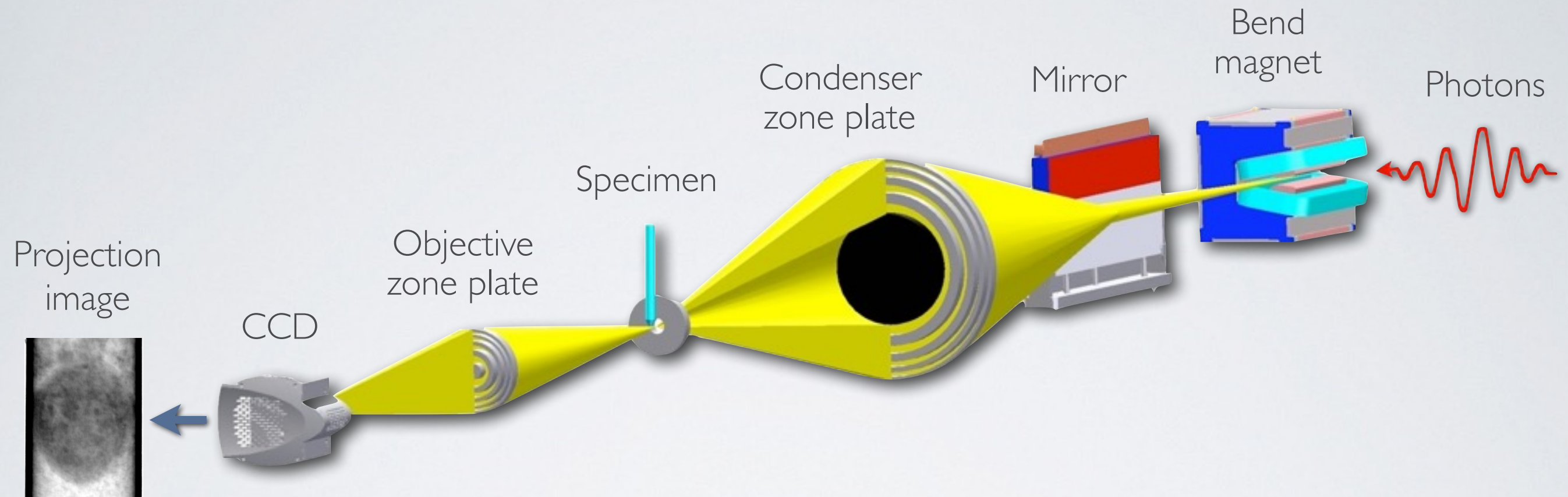


X-ray
microscope
end station

Specimen stage



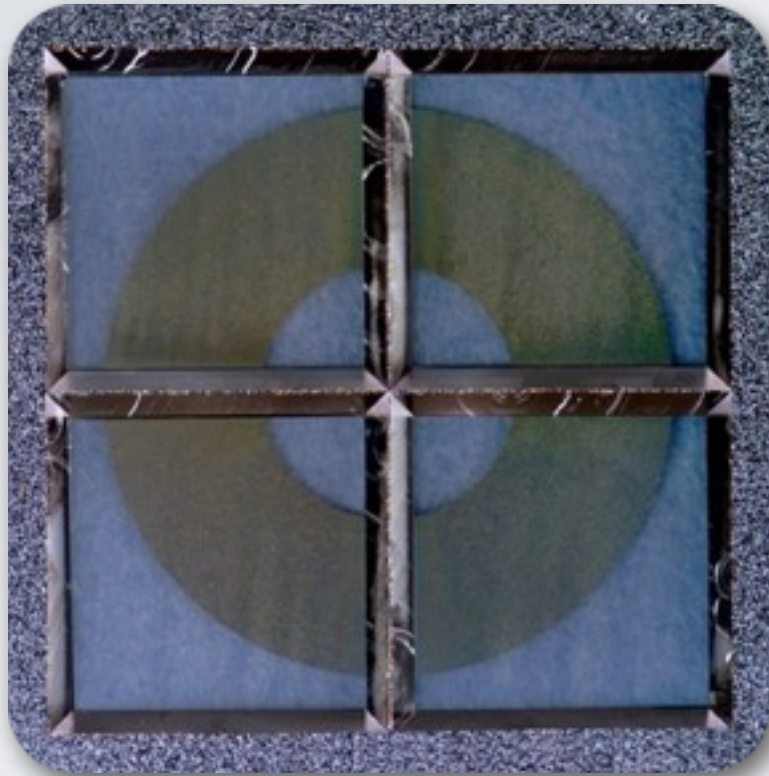
Soft x-ray tomography



- $2.4 \text{ nm } \lambda$ (517 eV)
- Condenser zone plate focuses source onto specimen
- Objective zone plate magnifies object onto CCD camera

Zone plate lenses - diffractive optics

Condenser lens



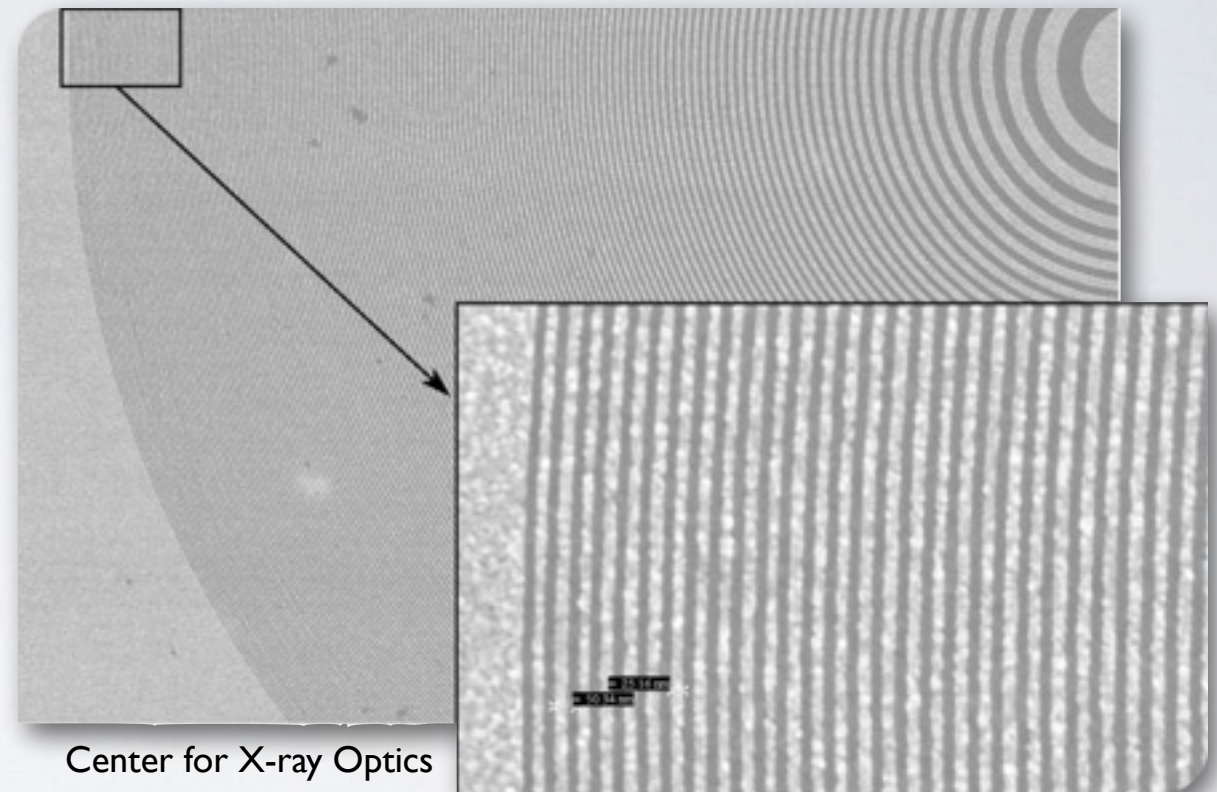
Diameter = 1 cm

No. of zones = 41,700

Outer zone width = 50 nm

Central stop diameter = 5 mm

Objective lens



Diameter = 63 μm

No. of zones = 628

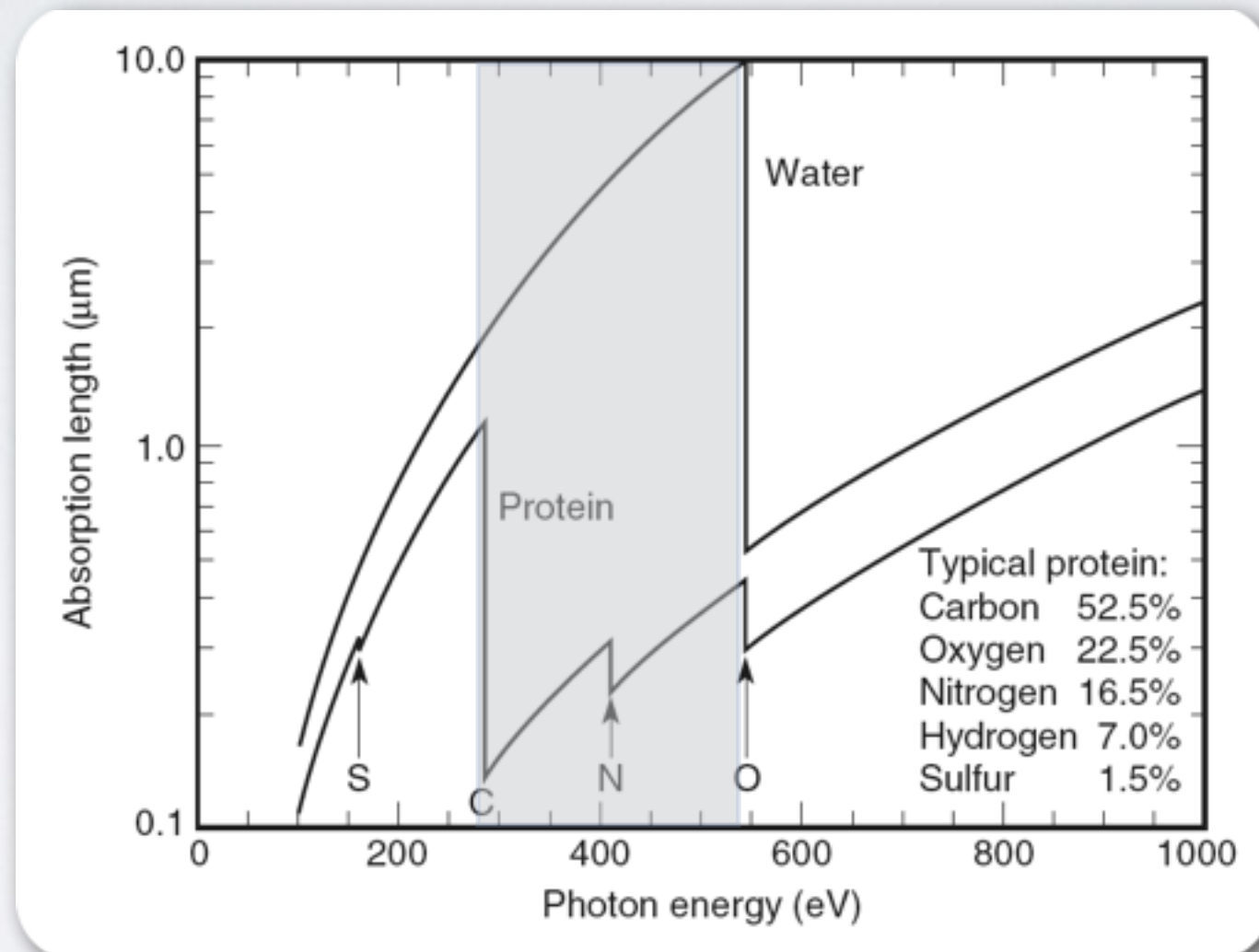
Outer zone width = 25 nm

Nickel plating

Imaging in the water window

Image between K shell absorption edges of C (284 eV, 4.4nm) & O₂ (543 eV, 2.3nm)

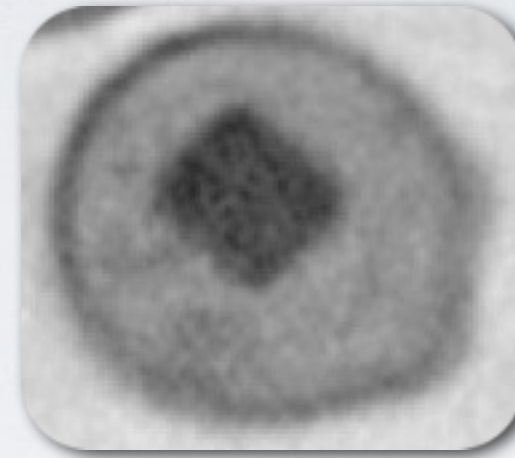
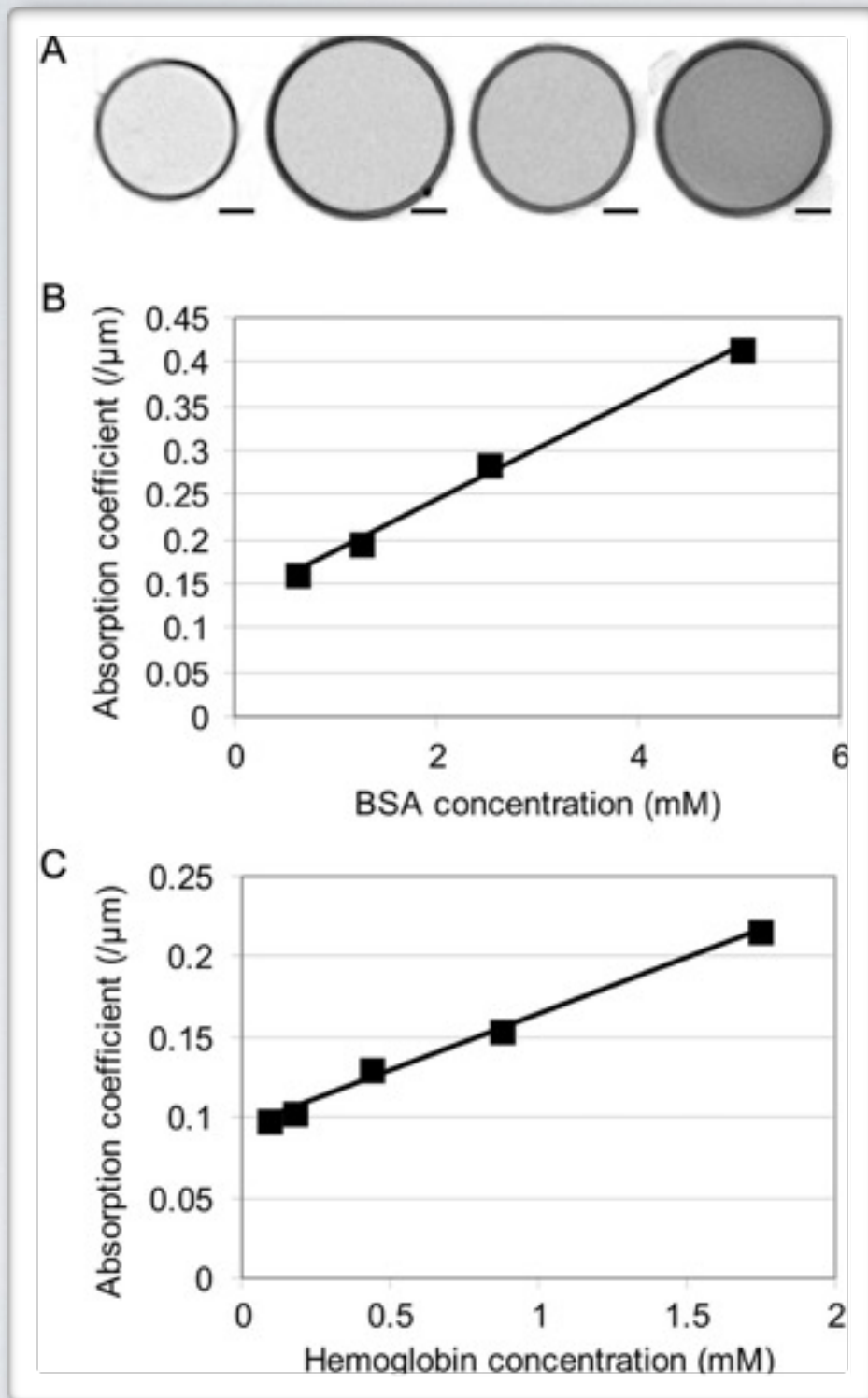
Absorption adheres to Beer-Lambert's law and is linear with thickness & concentration



2.4 nm

517 eV

Linear absorption coefficient



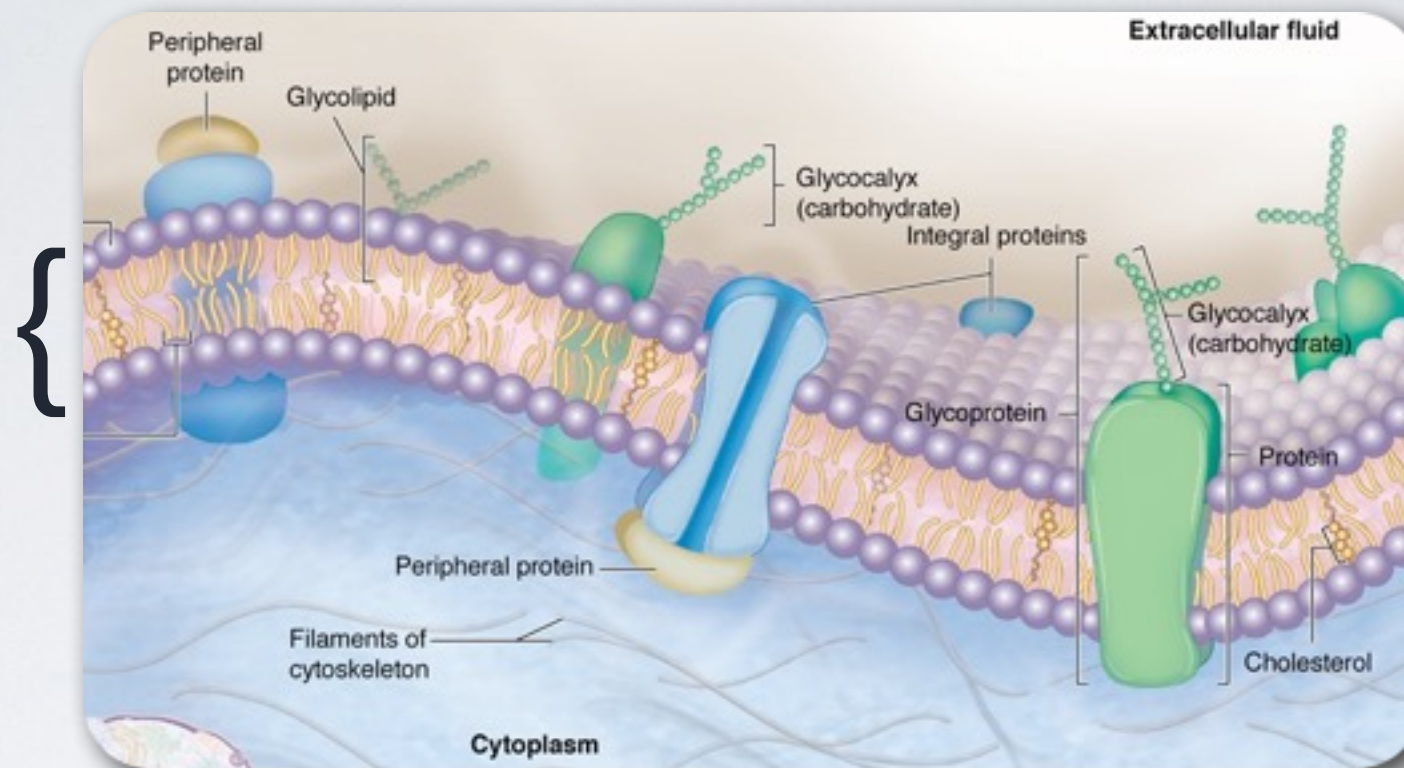
Alcohol oxidase
crystal in yeast cell

Calculated LAC $\Rightarrow 0.625 \mu\text{m}^{-1}$

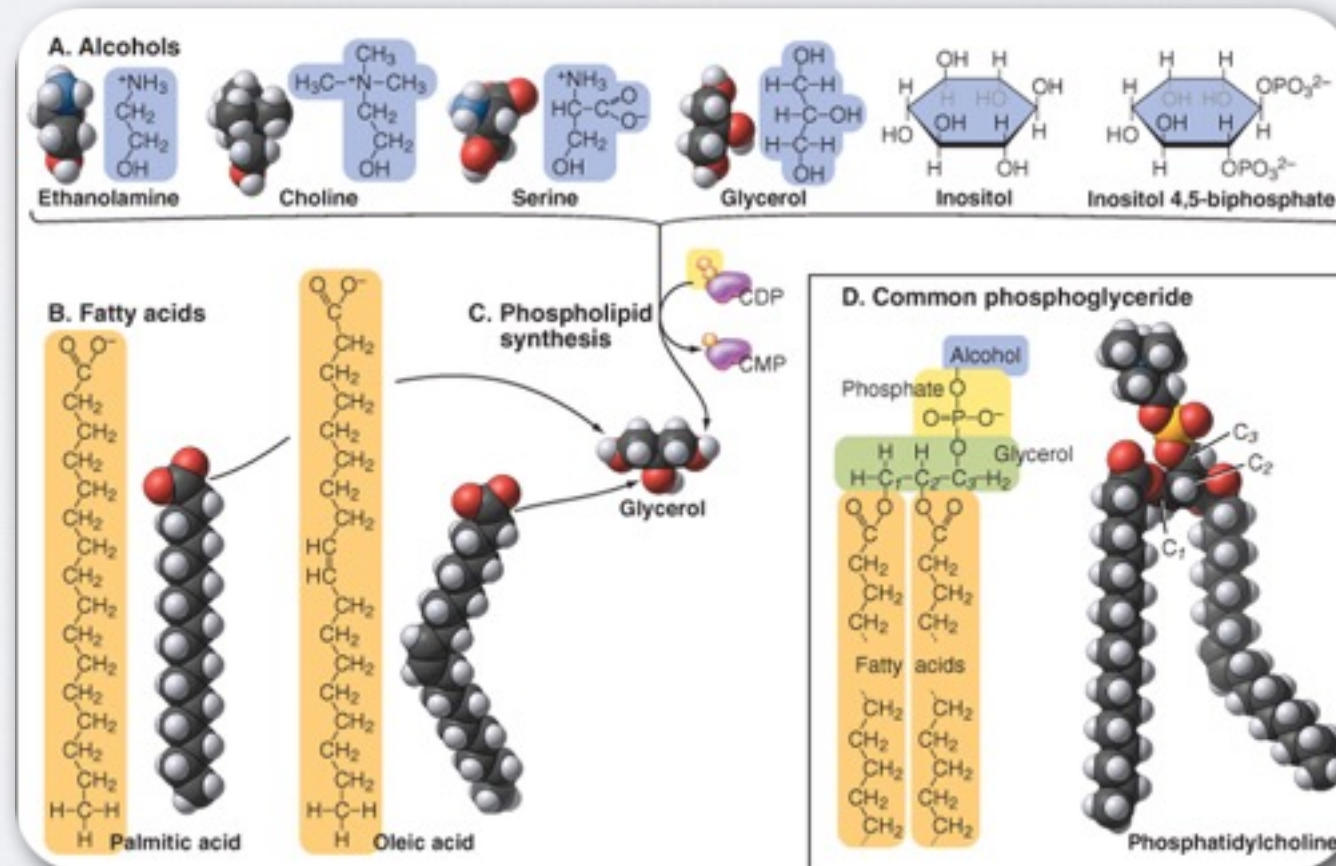
Measured LAC $\Rightarrow 0.626 \mu\text{m}^{-1}$

Imaging in the water window

Membrane
(lipid bilayer)

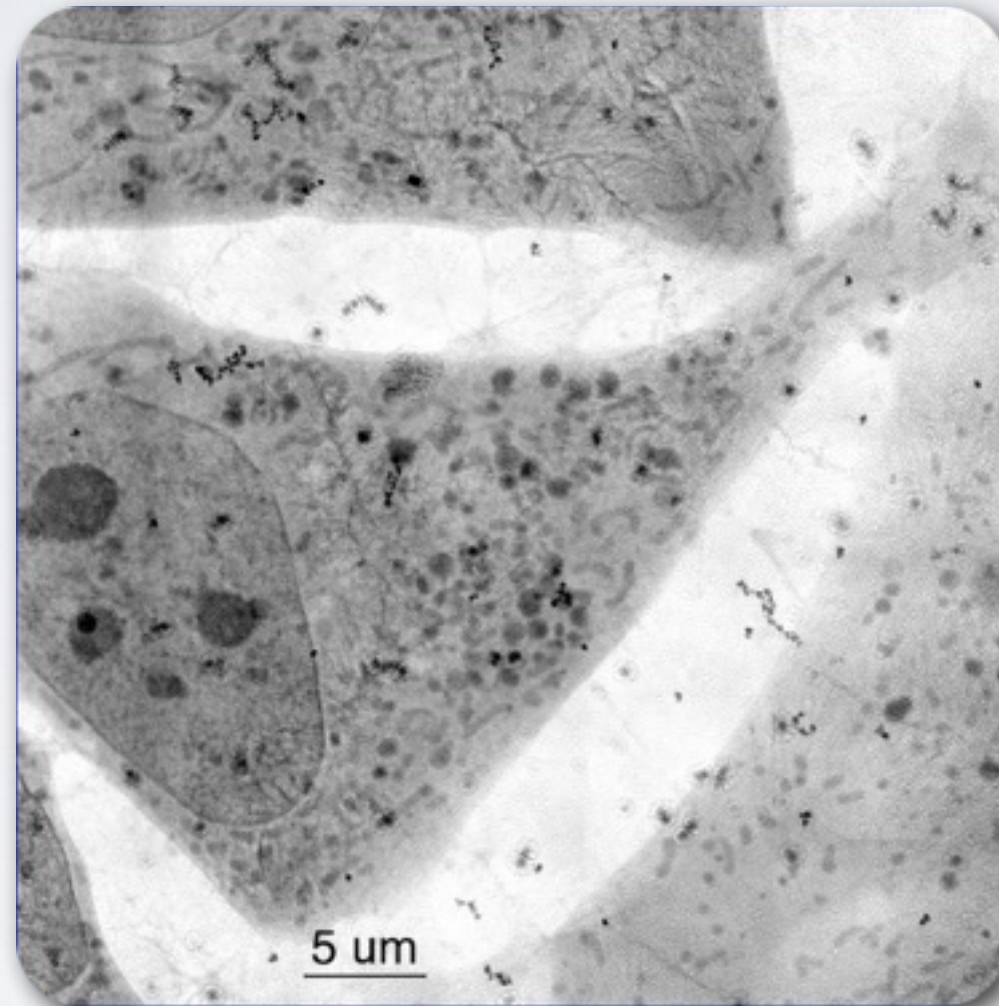


Membrane lipids
tightly packed
carbon molecules



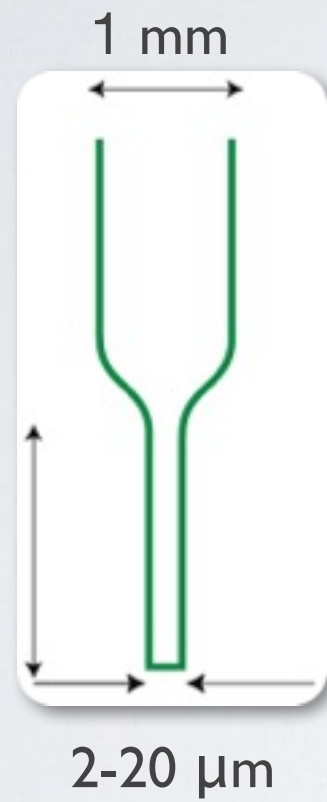
Imaging in the water window

High carbon content structures have high contrast



Specimen preparation

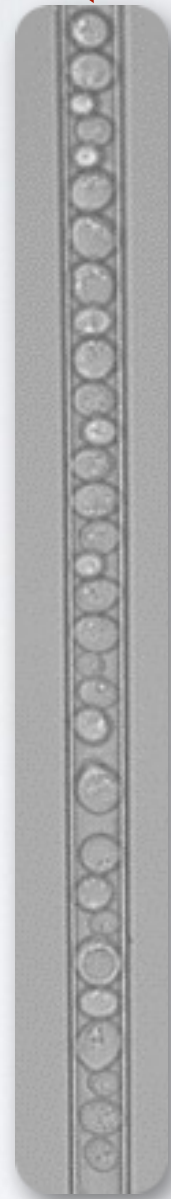
Specimen holder



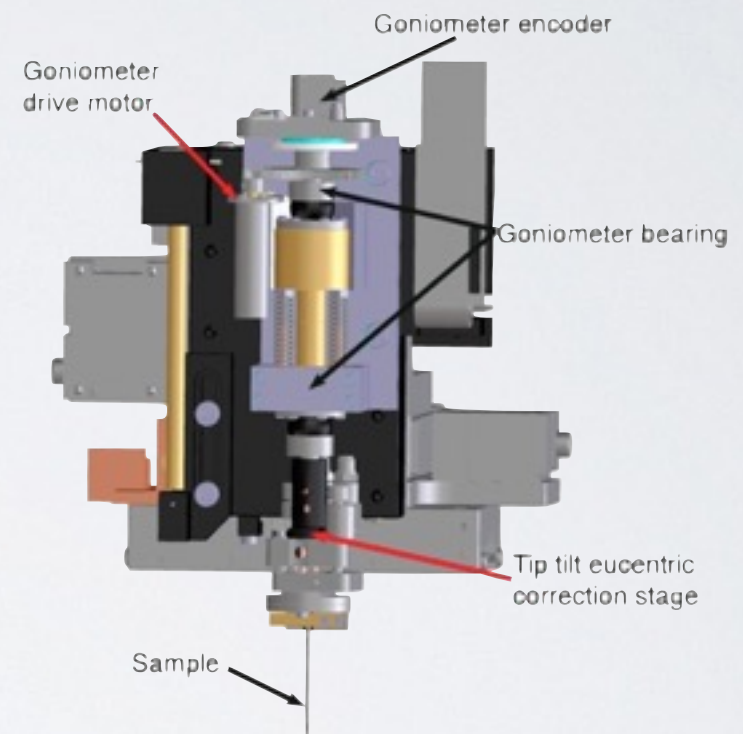
Specimen



Rapidly freeze



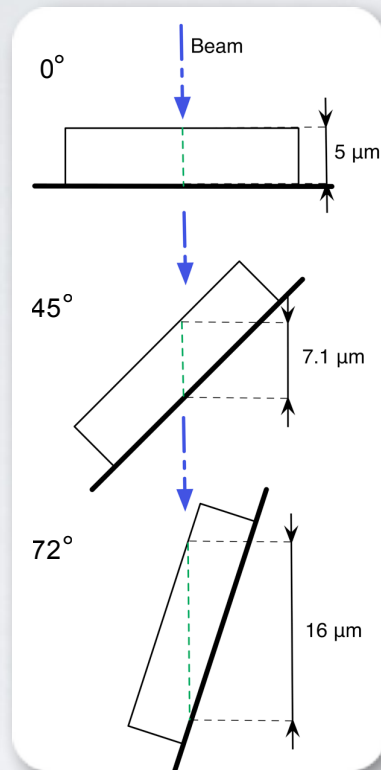
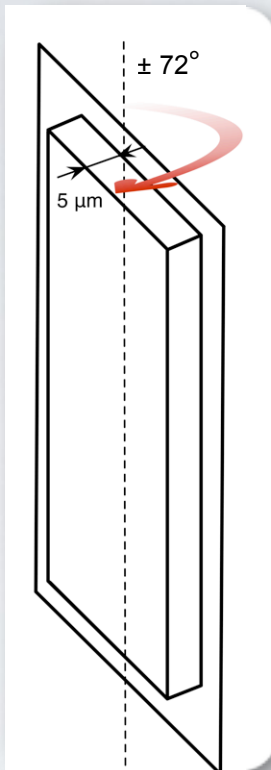
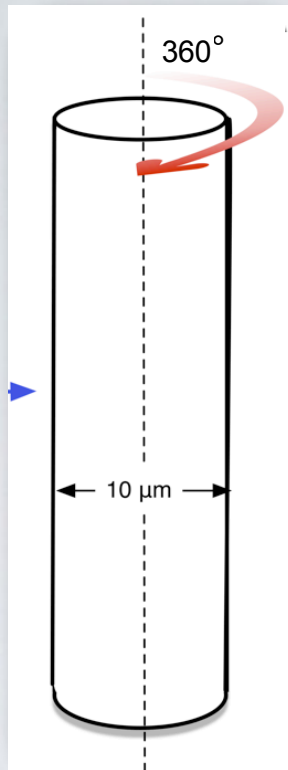
Fast - 5 min / cell



Full rotation vs. limited tilt

Full rotation
($\pm 90^\circ$)

Flat specimen
limited tilt

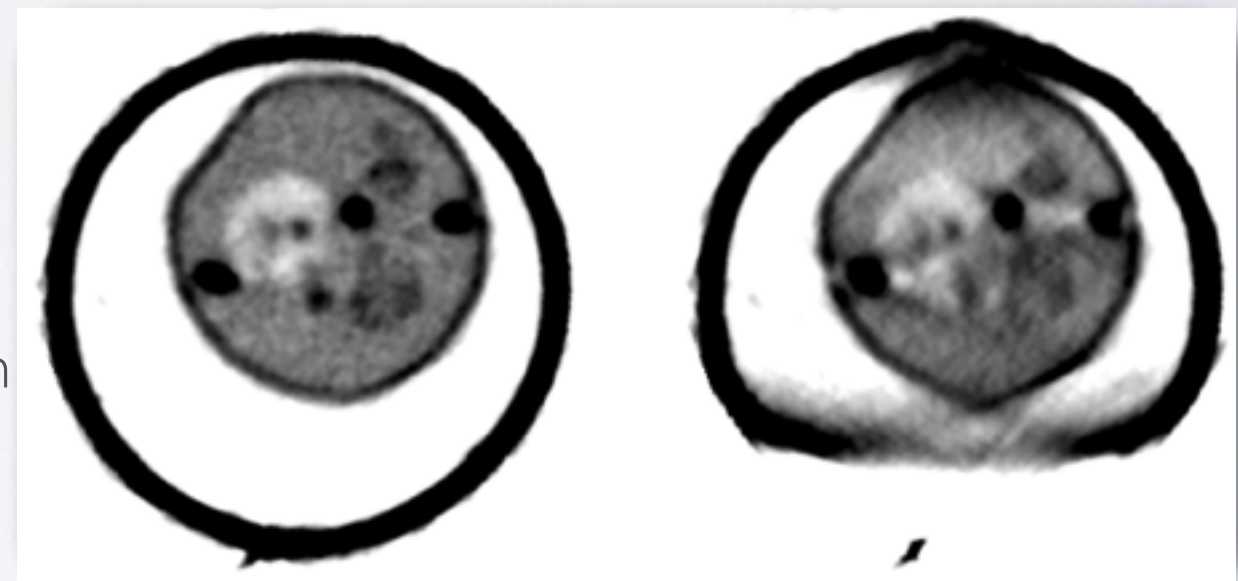
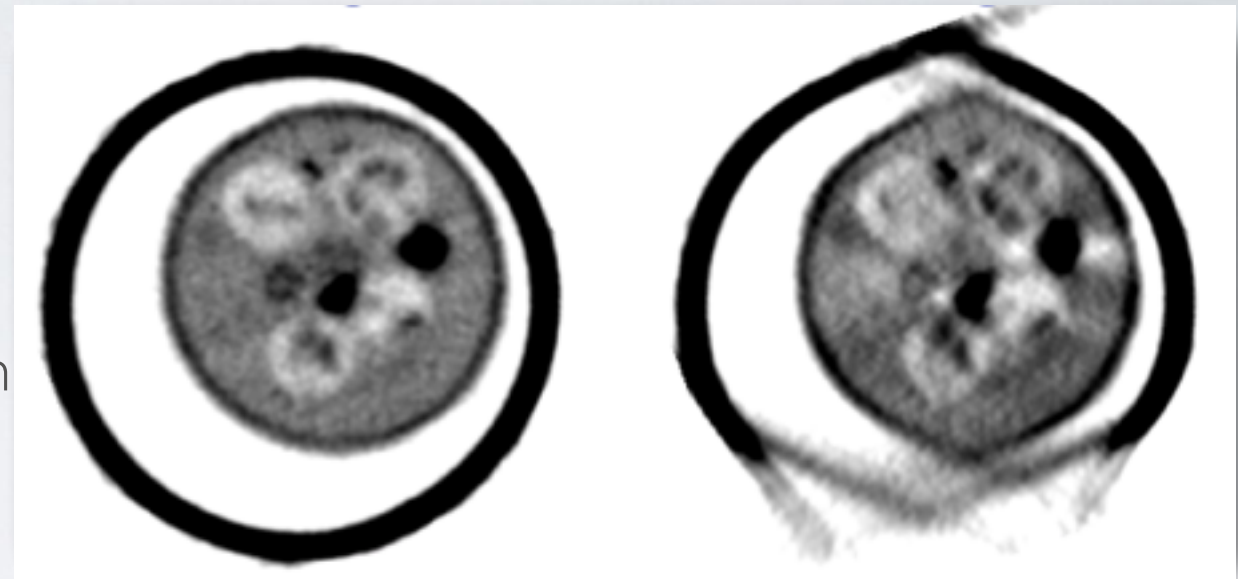


Filtered back
projection
reconstruction

Iterative
algorithm
reconstruction

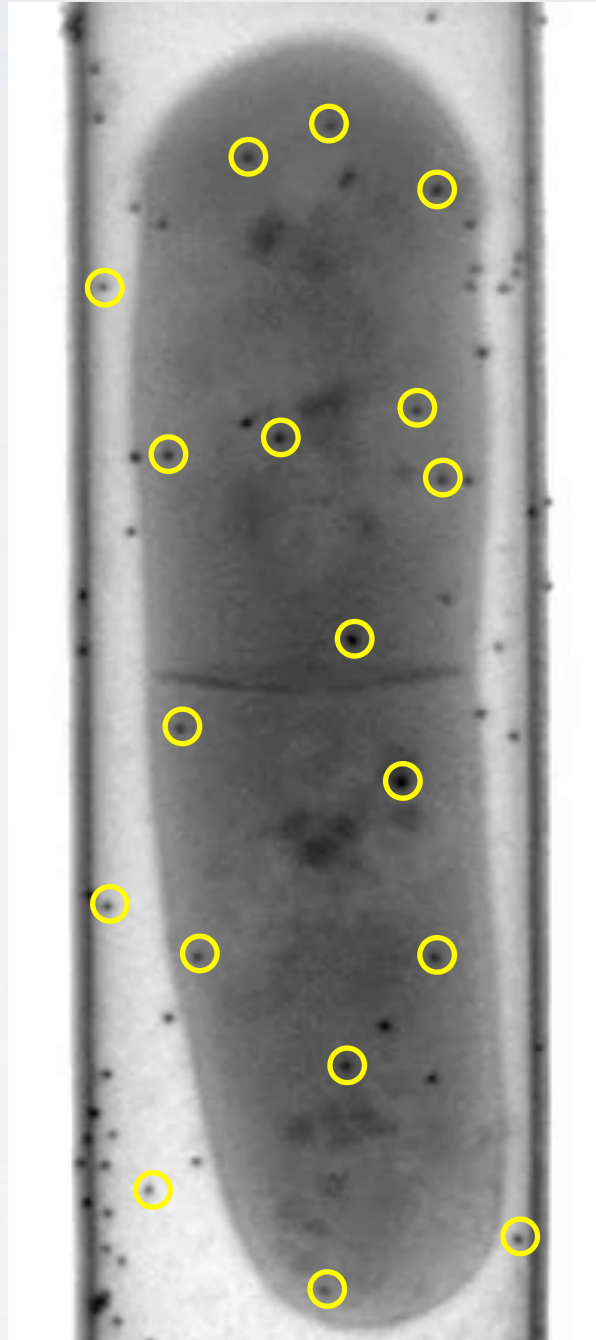
Full rotation
($\pm 90^\circ$)

Limited tilt
($\pm 70^\circ$)



Aligning projection images

Gold particles to align images



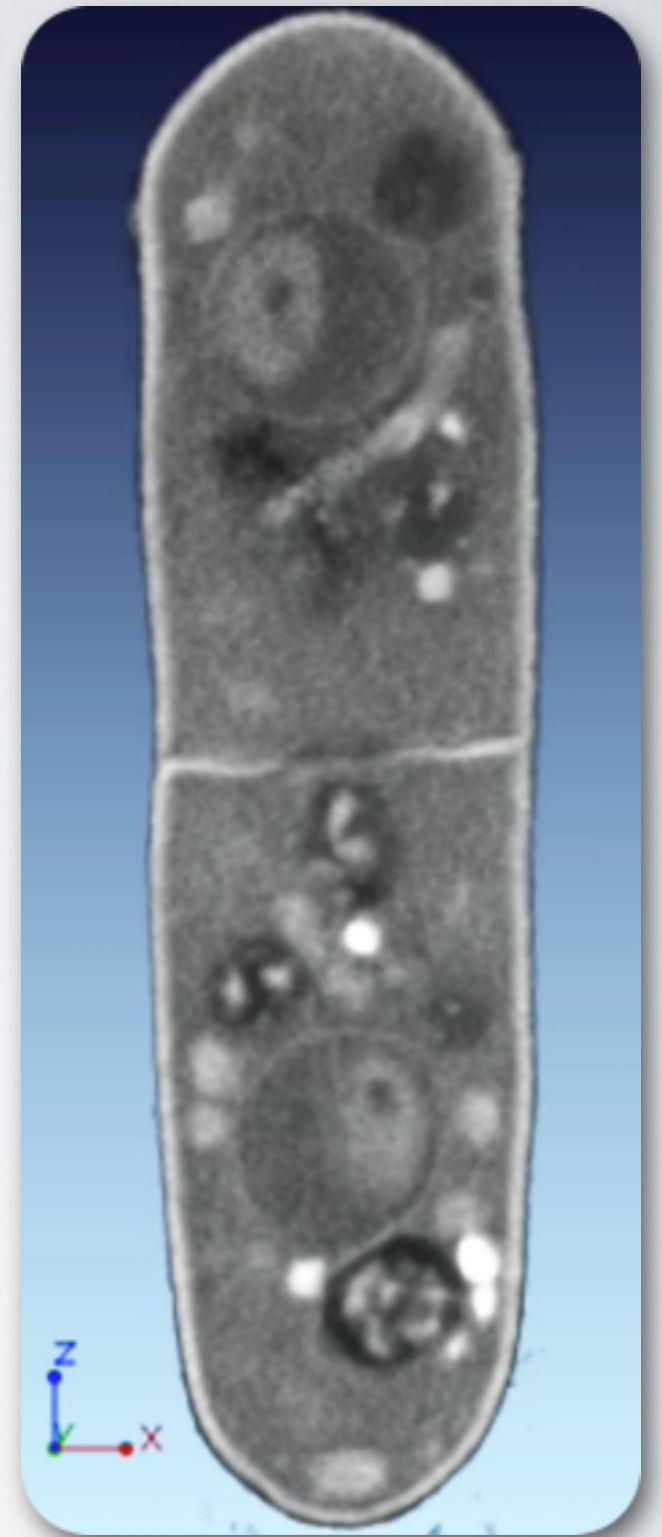
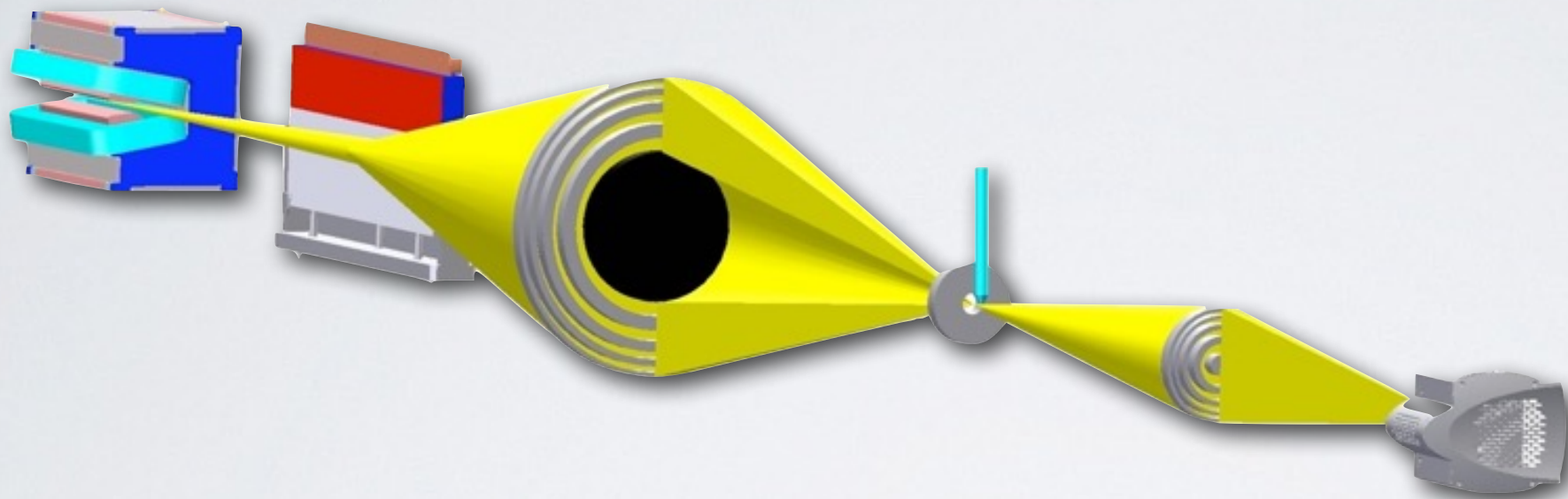
Tomographic reconstruction

- Filtered back projection
- Iterative algorithms

Orthoslices from tomographic reconstruction



Negative images



Segmentation

S. pombe organelles segmented, color-coded



Nucleolus

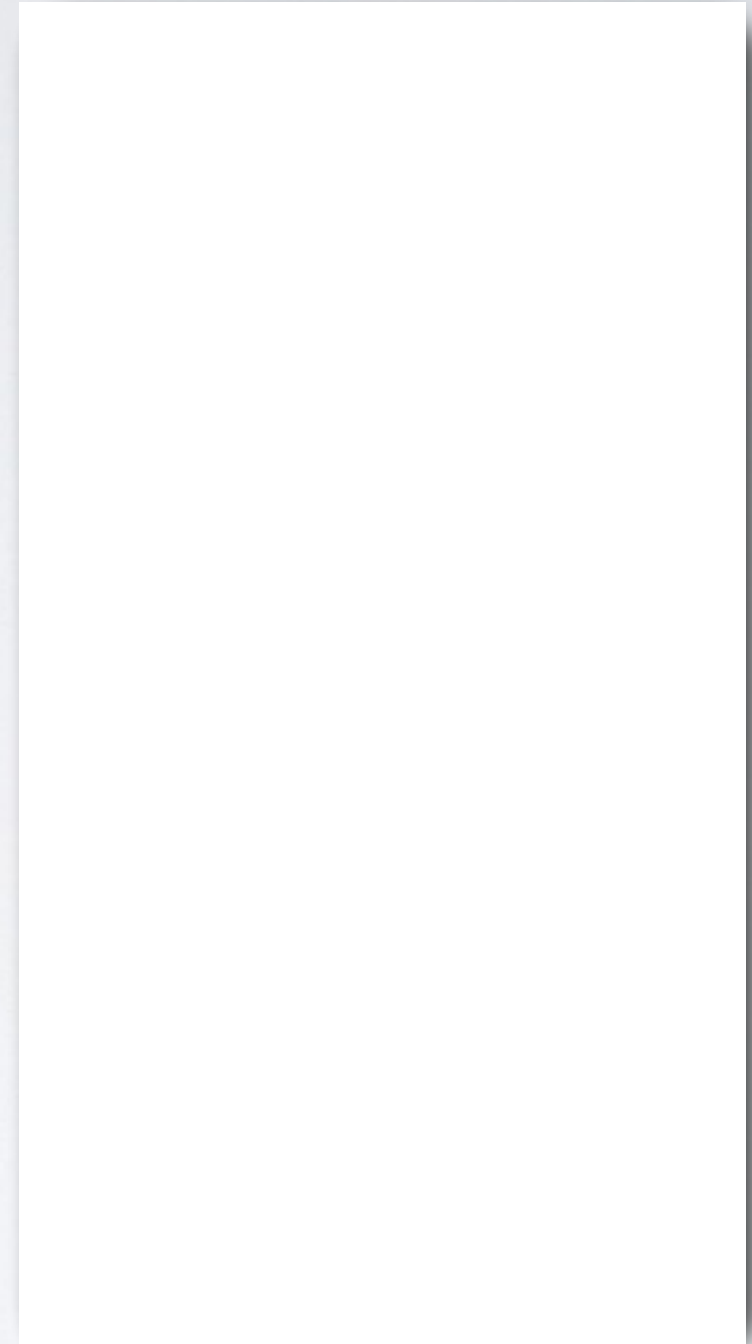
Nucleus

Lipids

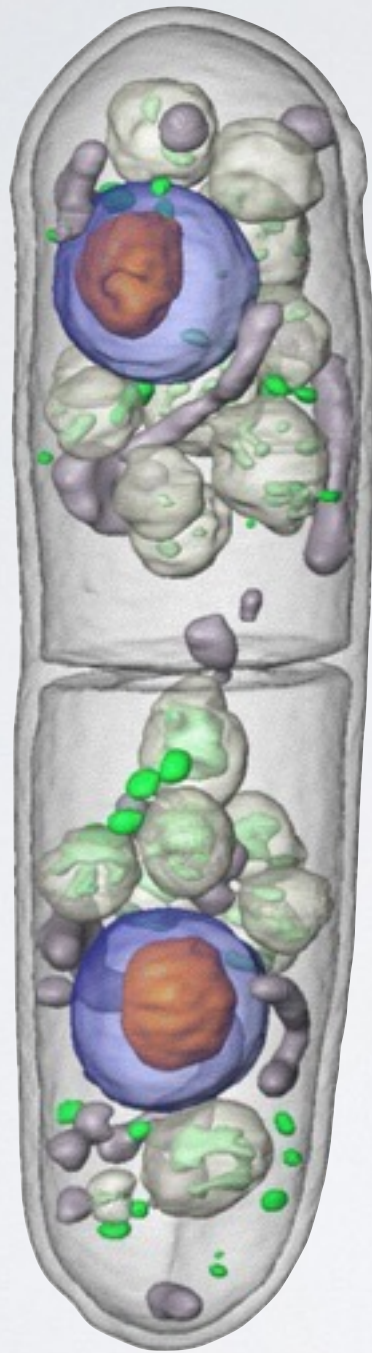
Mitochondria

Vacuoles

**Contents of
vacuoles**



S. pombe organelles - quantitative data

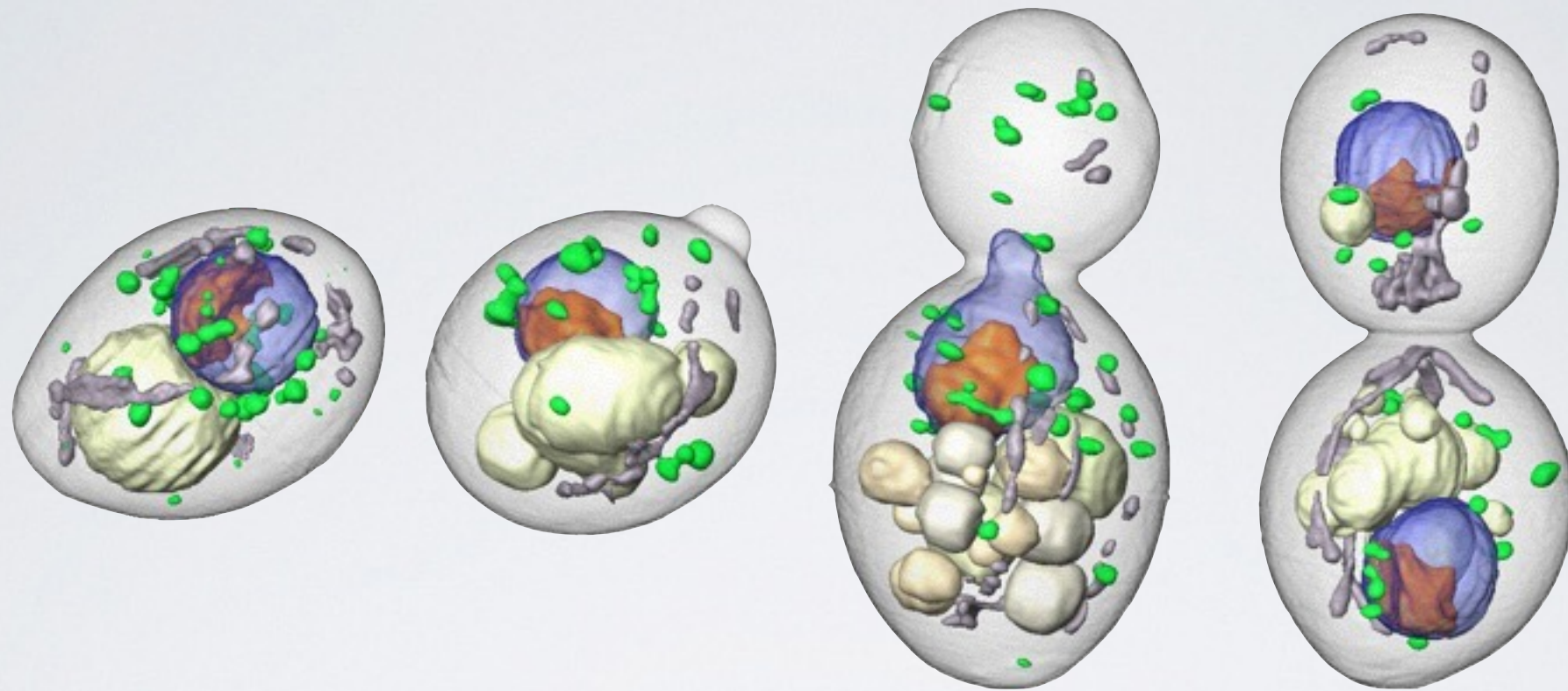


	Volume (μm^3)	Average LAC (μm^{-1})
Lipids	0.45	0.72
Mitochondria	2.97	0.42
Nuclei	4.59, 4.90	0.31
Nucleoli	0.74, 0.71	0.37
Endosomes	13.9	0.23
Endosome inclusions	1.15	0.42

Phenotypic consequences of genetic manipulations

Normal structure of *S. cerevisiae*

Diploid



G1

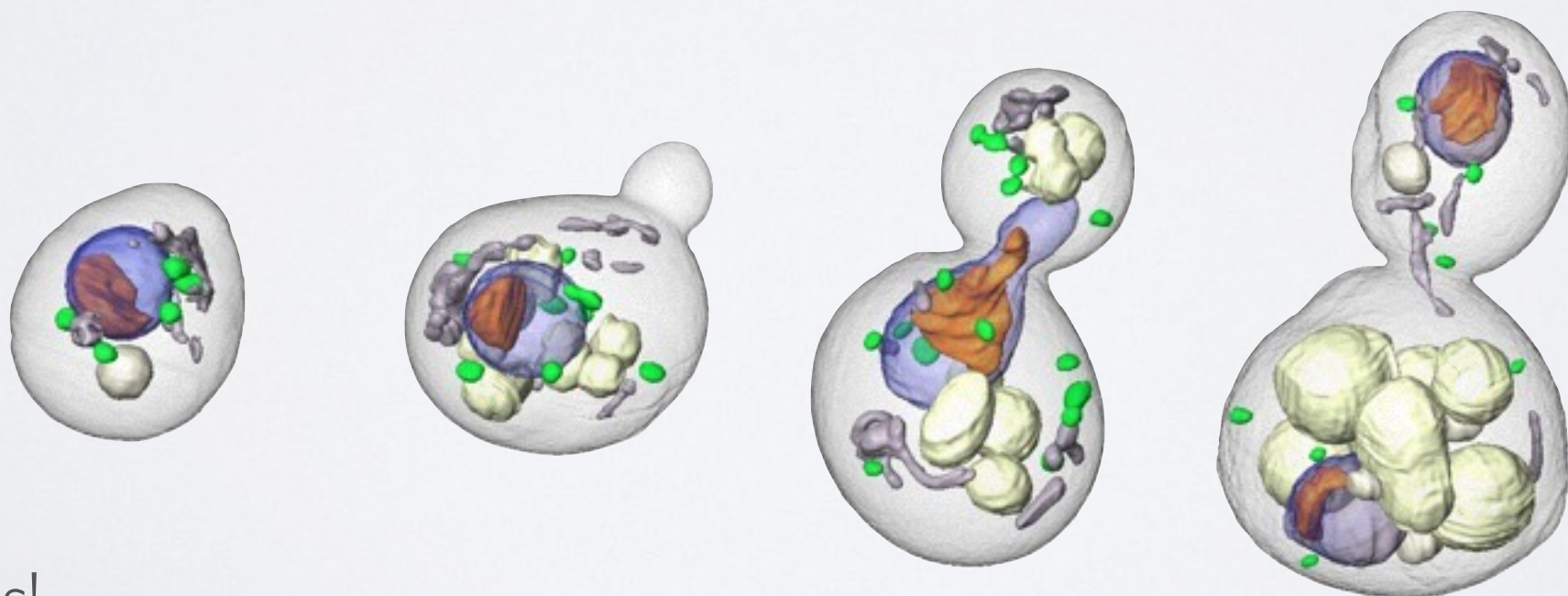
S

G2

M



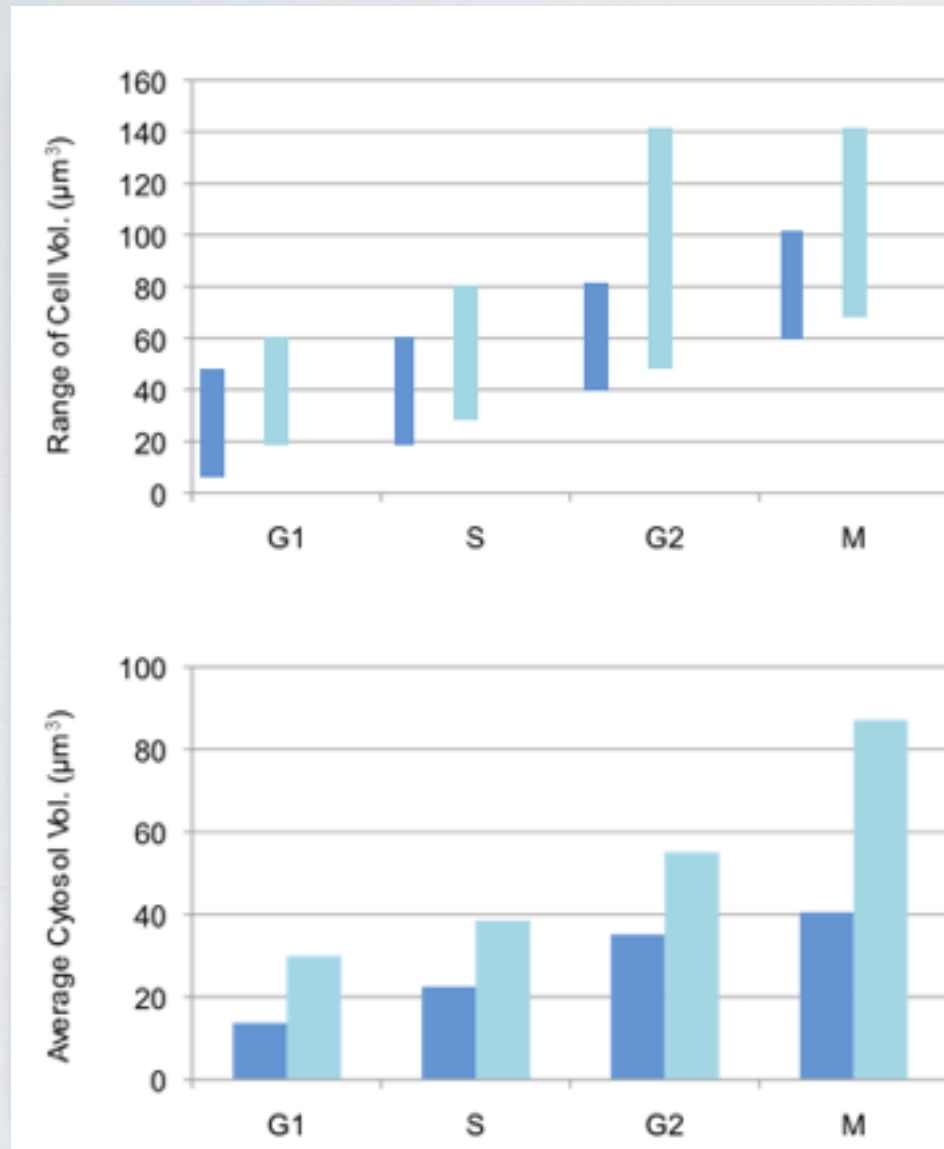
Haploid



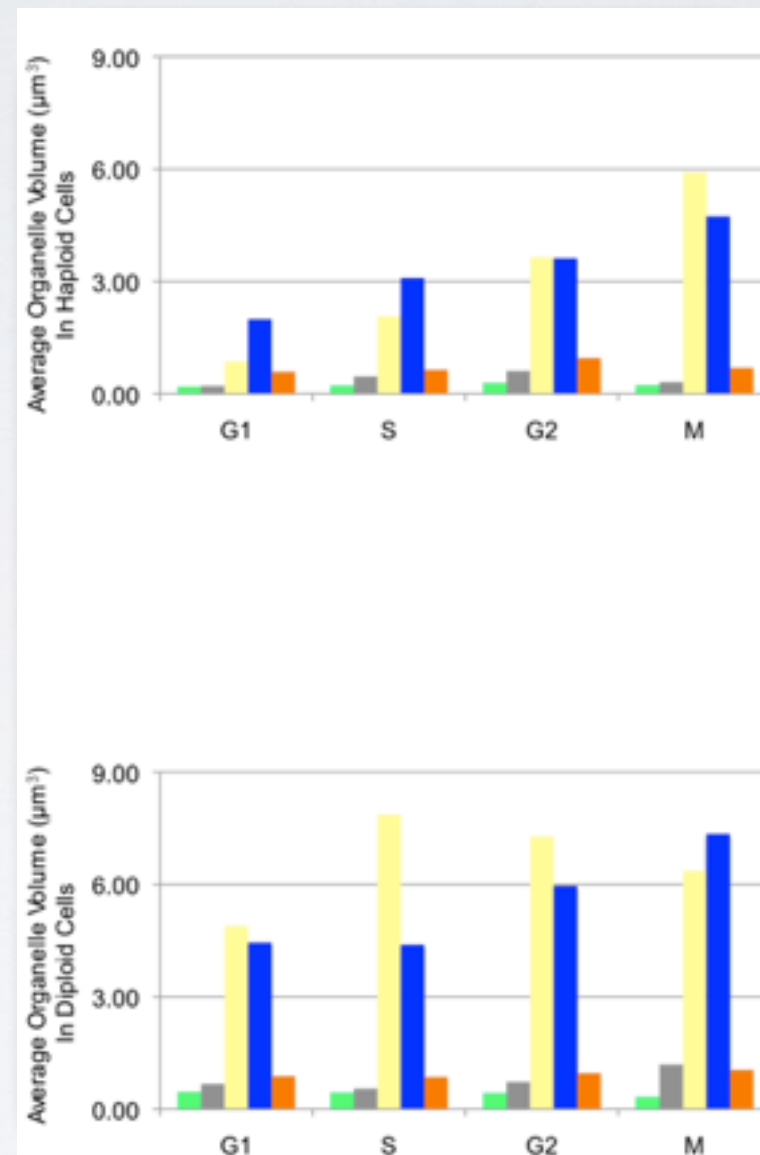
250 cells!

Normal structure of *S. cerevisiae*

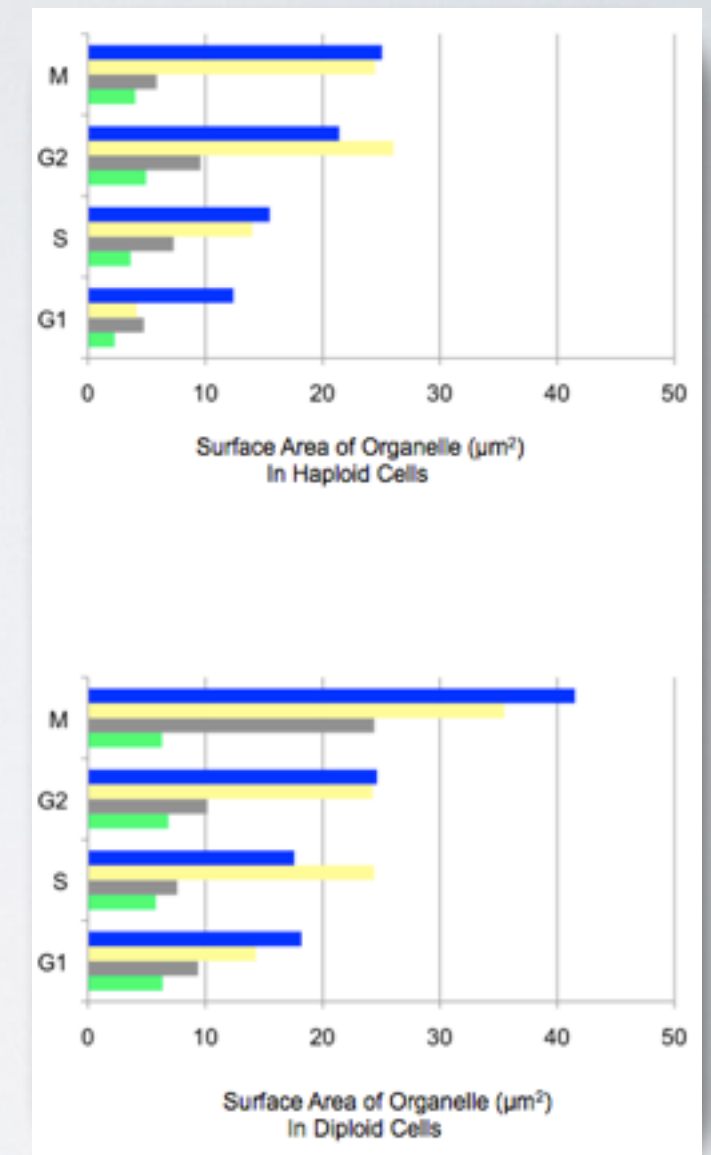
Cell volume



Organelle volume



Organelle surface area



Gene knockouts affecting mitochondria

Wildtype

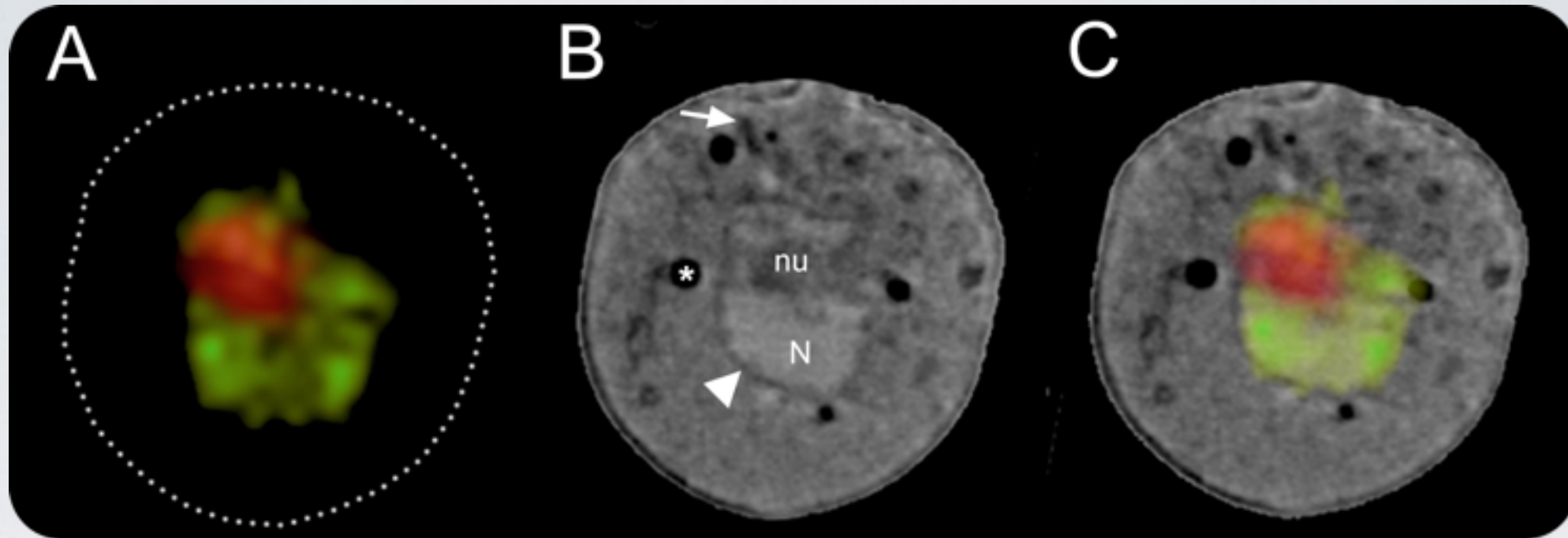
dnm1 KO

fzo1 KO

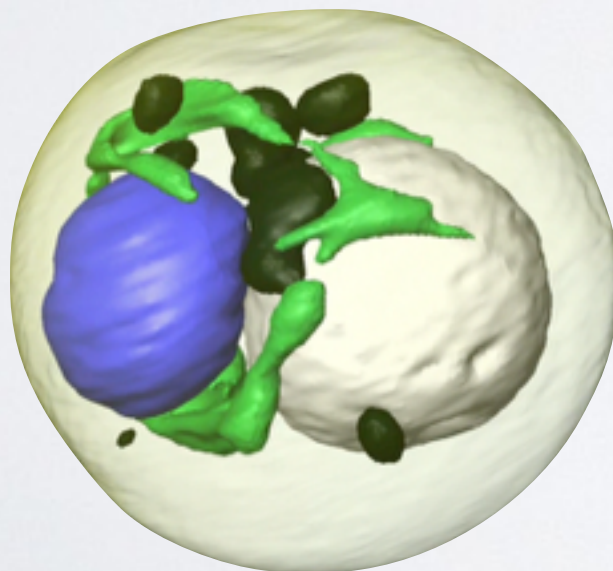


Jennifer Lippincott-Schwartz, NIH
Arnold Seo, NIH

Regulation of nucleus size and shape



Cinquin BP, Do M, McDermott G, Walters AD, Myllys M, Smith EA, Cohen-Fix O, Le Gros MA and Larabell CA. (2014). J. Cellular Biochemistry. 115(2):209-216.



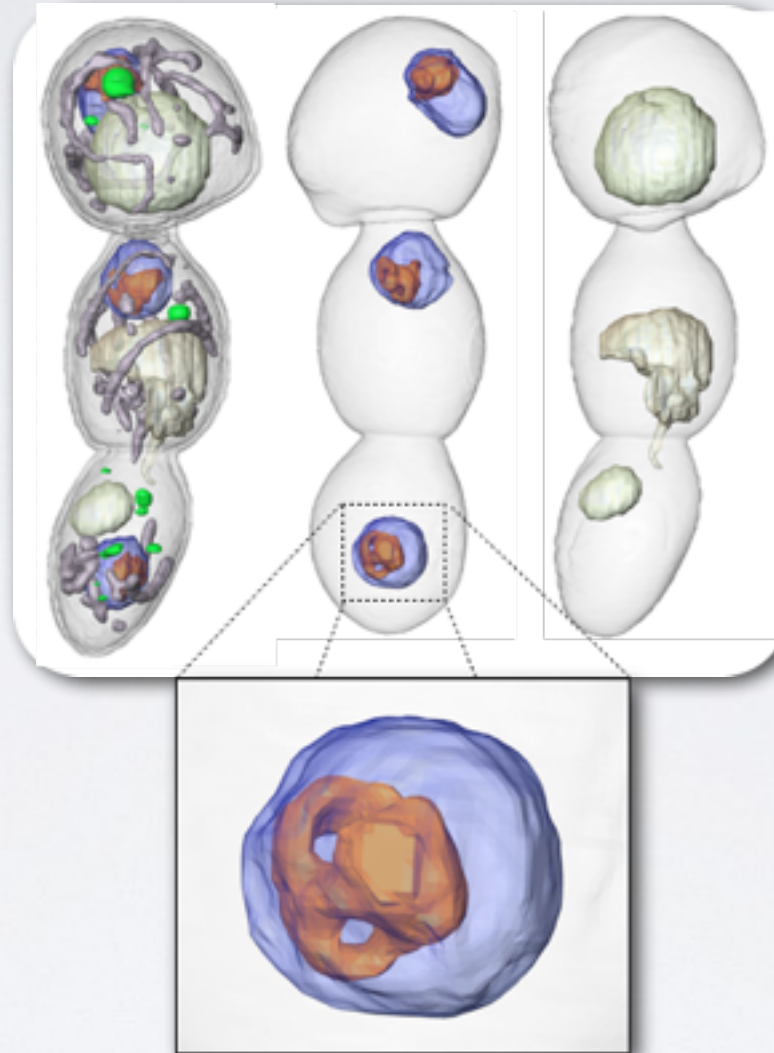
Walters, A.D., May, C.K., Dauster, E., Cinquin, B.P., Smith, E.A., Robellet, X., D'Amours, D., Larabell, C.A., Cohen-Fix, O. (2014). The yeast polo kinase, Cdc5, regulates the shape of the mitotic nucleus. *Current Biology*. In press.

Effect of peptoids on pathogenic yeast

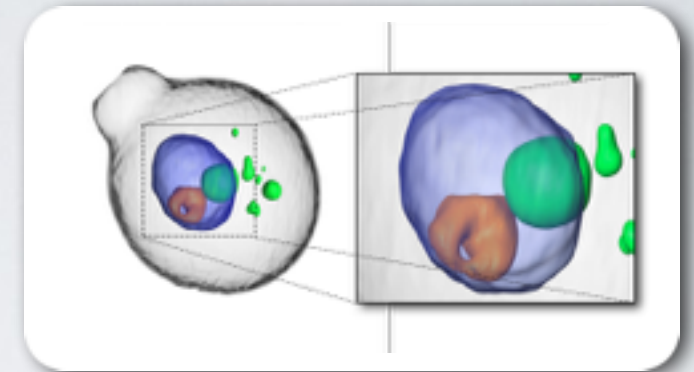
Pathogenic



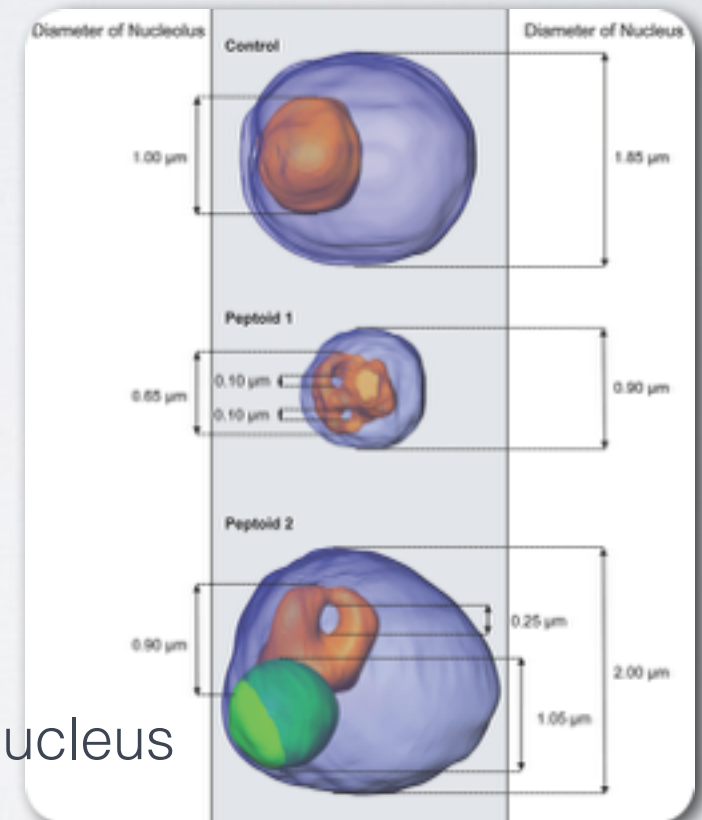
Peptoid 1 treated



Peptoid 2 treated



Effects on nucleus

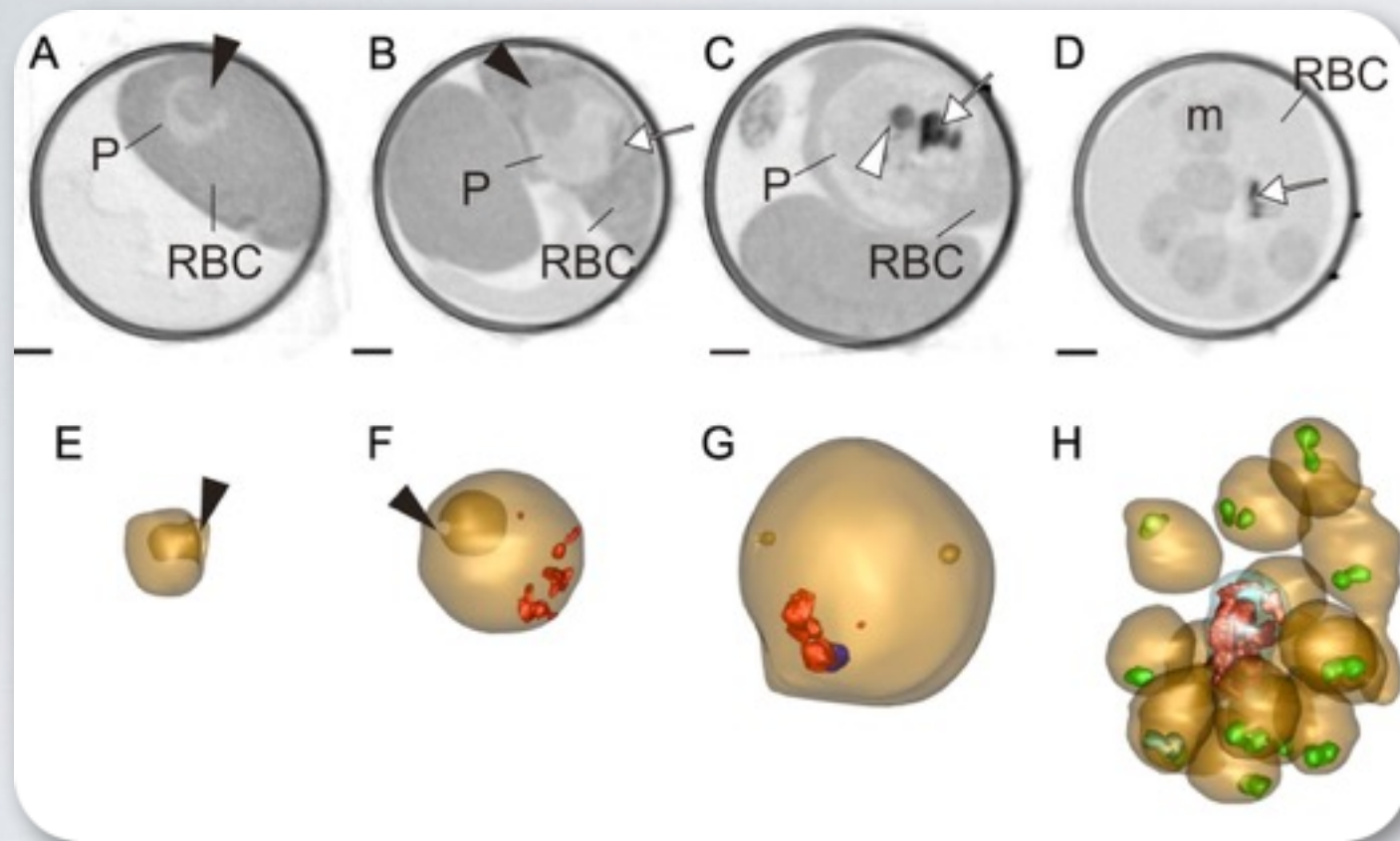


Lipid in nucleus

M Uchida, G McDermott, M Wetzler, MA Le Gros, M Myllys, C Knoechel, A Barron, CA Larabell. (2009). PNAS. 206(46):19375-19380

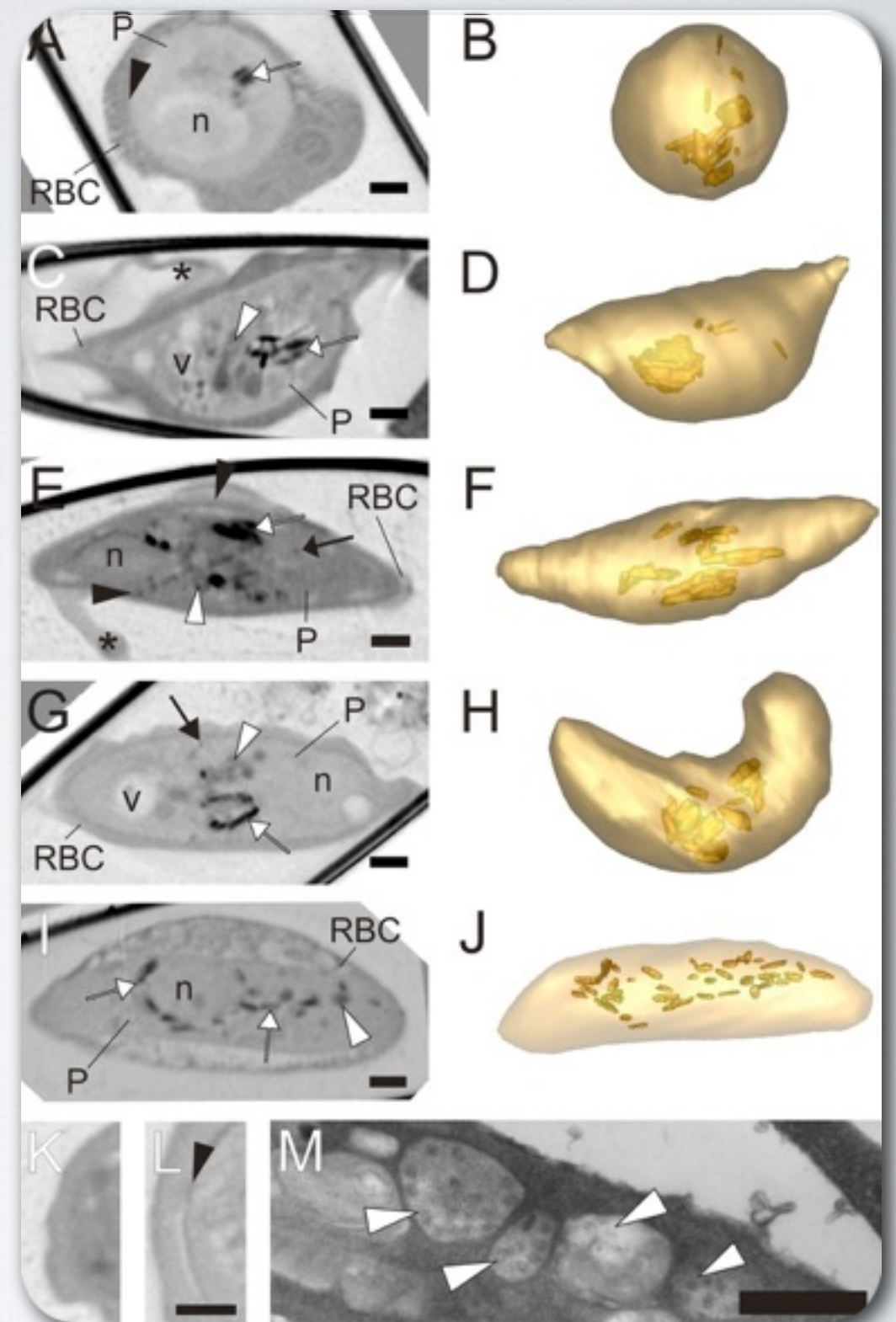
Host - parasite interactions

Sexual stage



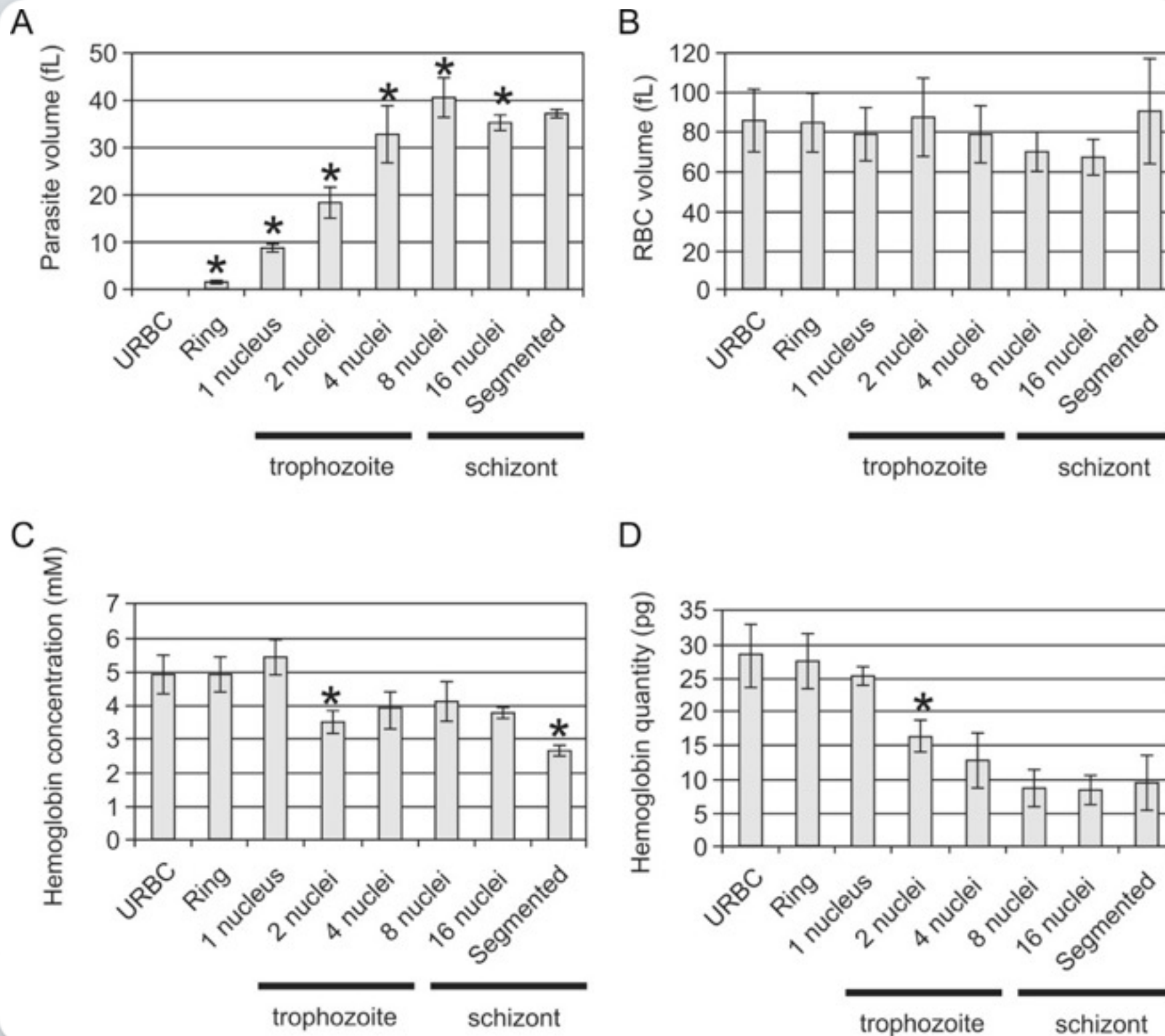
- Total volume of infected RBC remains constant
- Parasite occupies ~ 50% of RBC volume.
- 70% of RBC hemoglobin digested during parasite development

Asexual stage

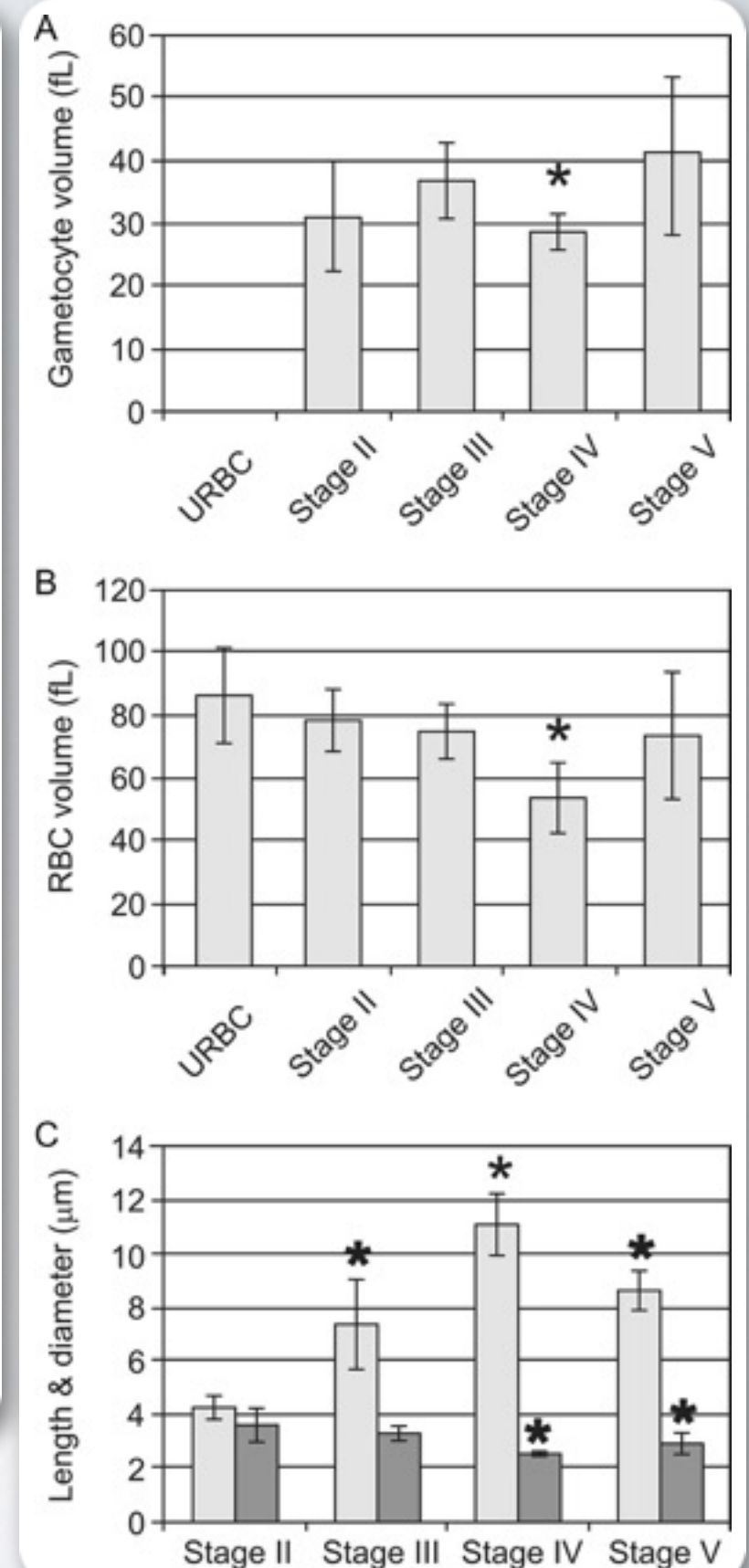


Malaria, *p. falciparum*

Sexual stage

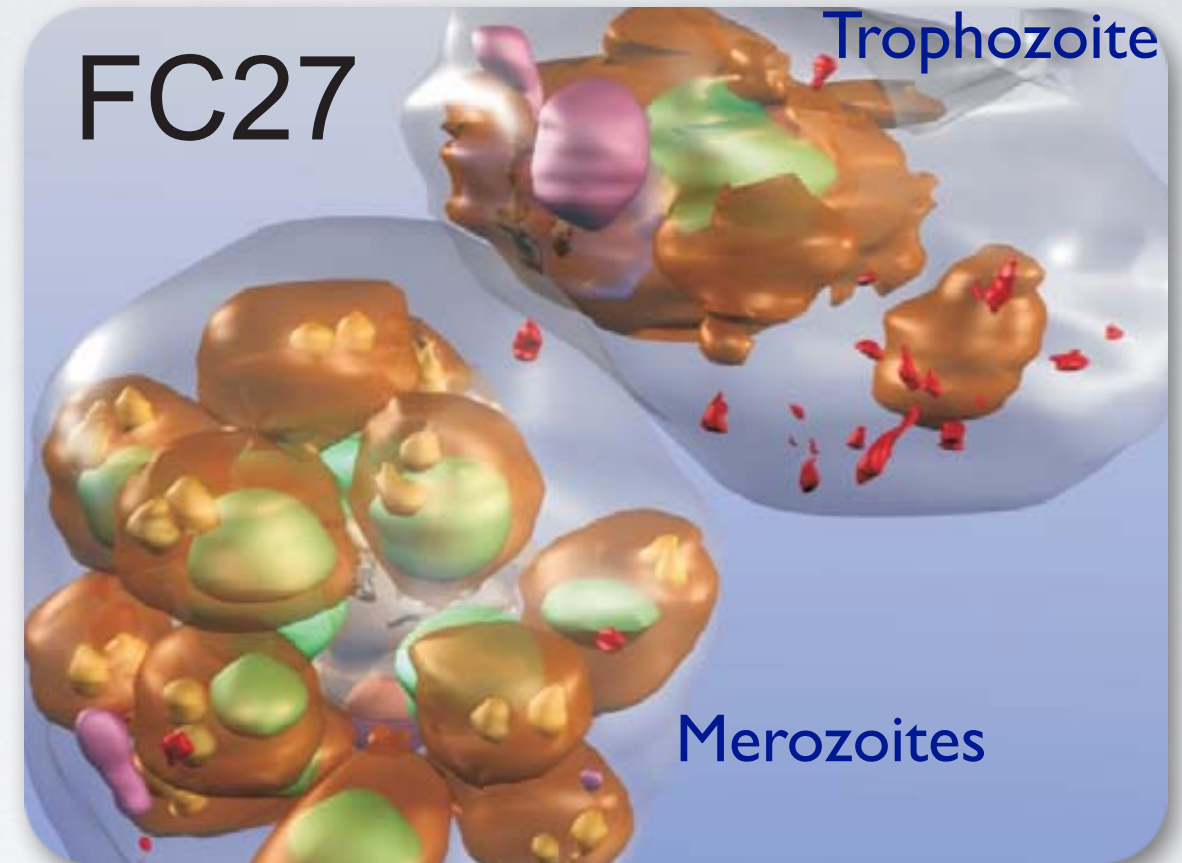
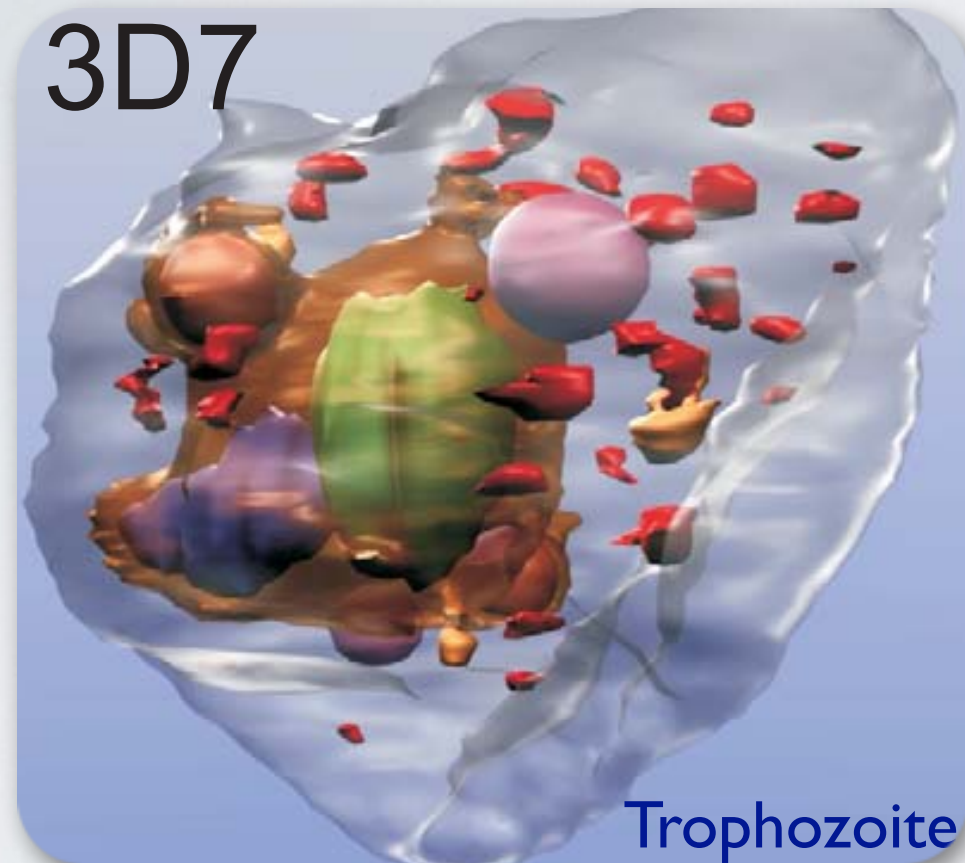


Asexual stage



Malaria, *p. falciparum*

How do parasite adhesion proteins get to blood cell surface?



- Parasite
- Nucleus
- Hemoglobin
- Maurer's clefts
- Rhoptry
- Digestive vacuole

E Hanssen, C Knoechel, N Abu Bakar, N Klonas, S Deed, MA Le Gros, CA Larabell & L Tilley, J. Structural Biology (2011) 173:161-168.

Lymphocytes

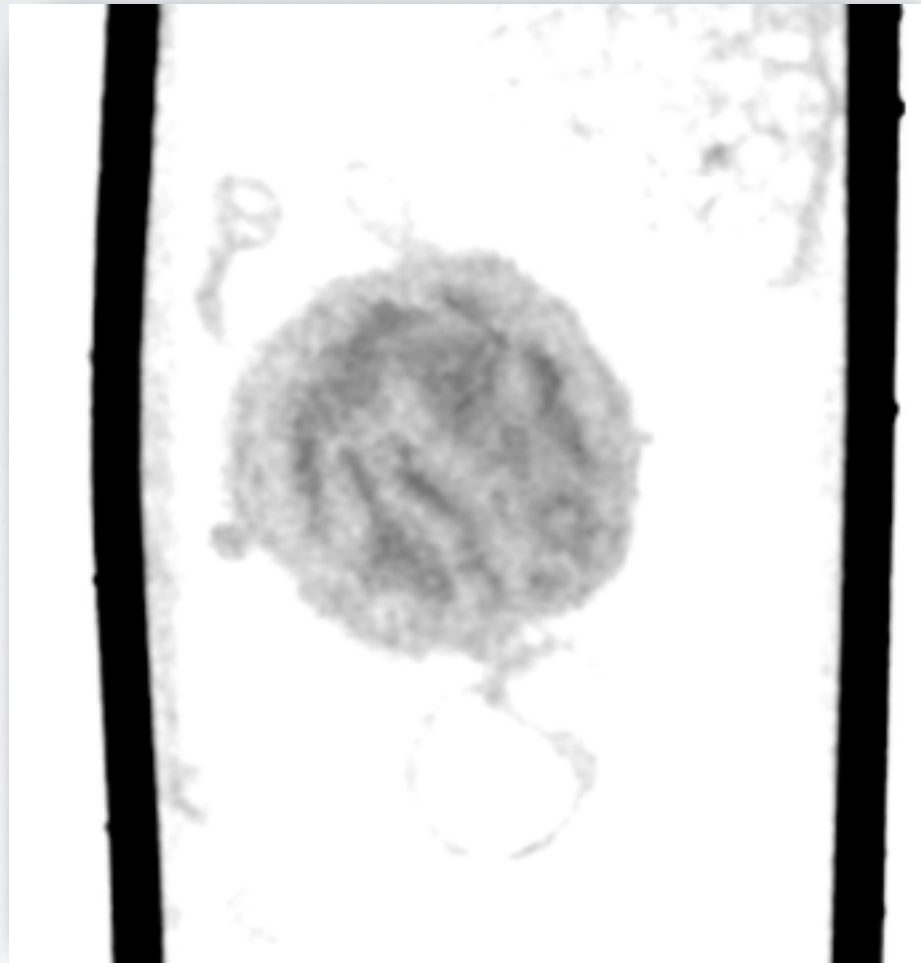
SXT of human lymphoblastoid cell (Encode GM12878)

Flipping through orthoslices

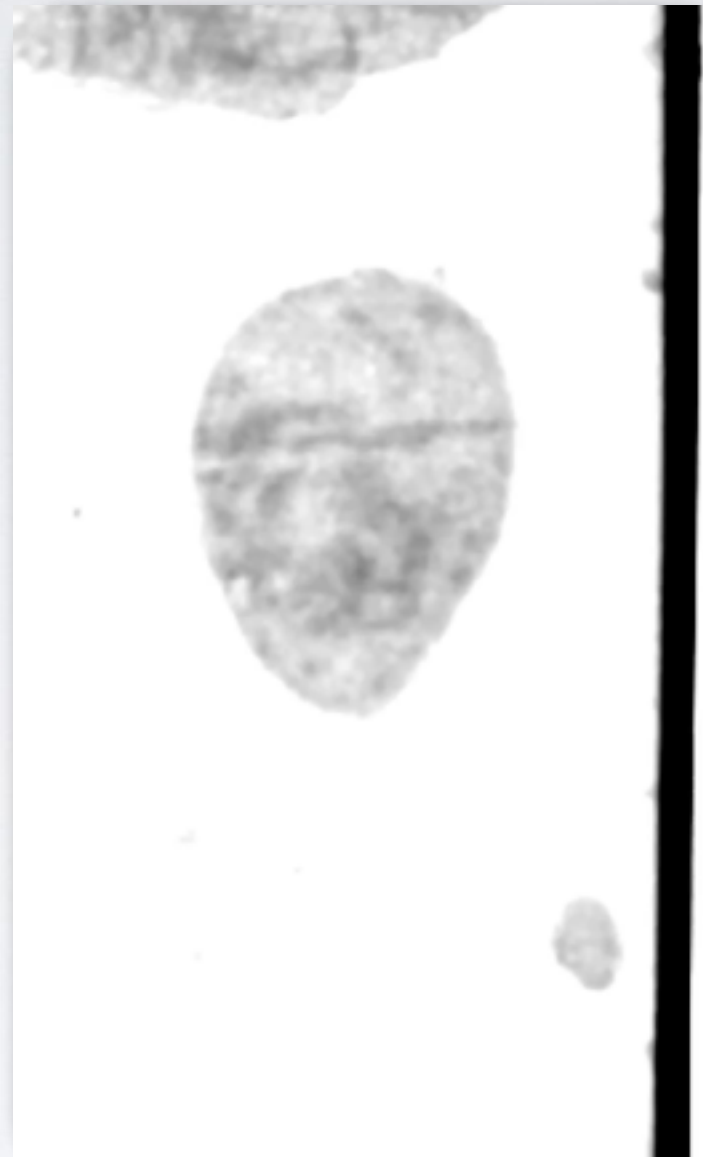


SXT of human lymphoblastoid cell (Encode GM12878)

Flipping through orthoslices

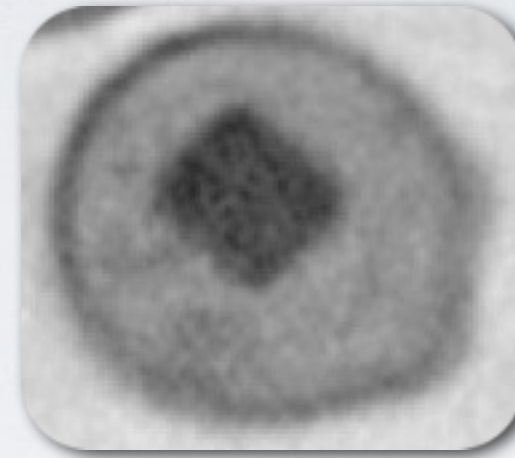
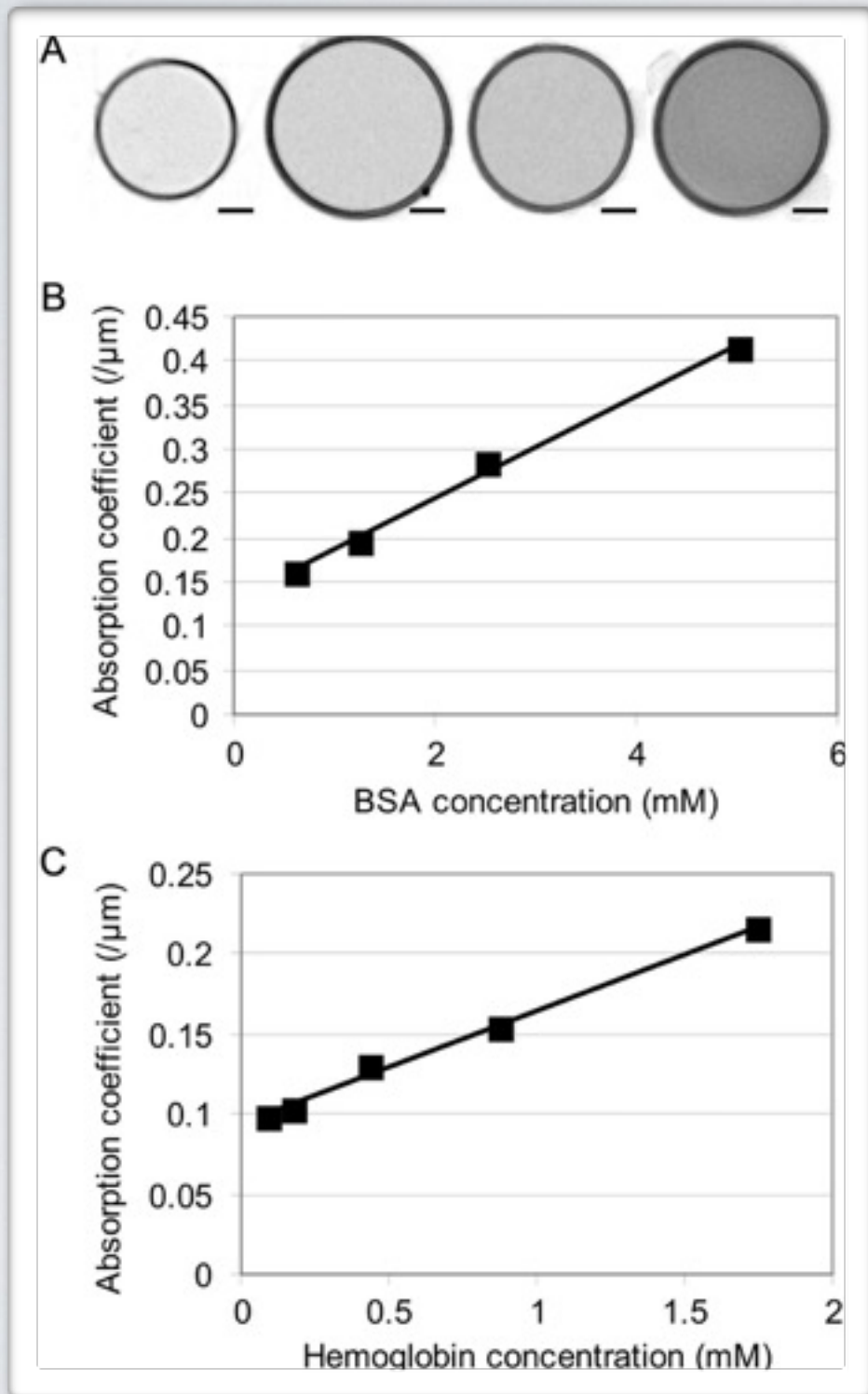


SXT of human lymphoblastoid cell (Encode GM12878)



Semi-automatic segmentation

Linear absorption coefficient



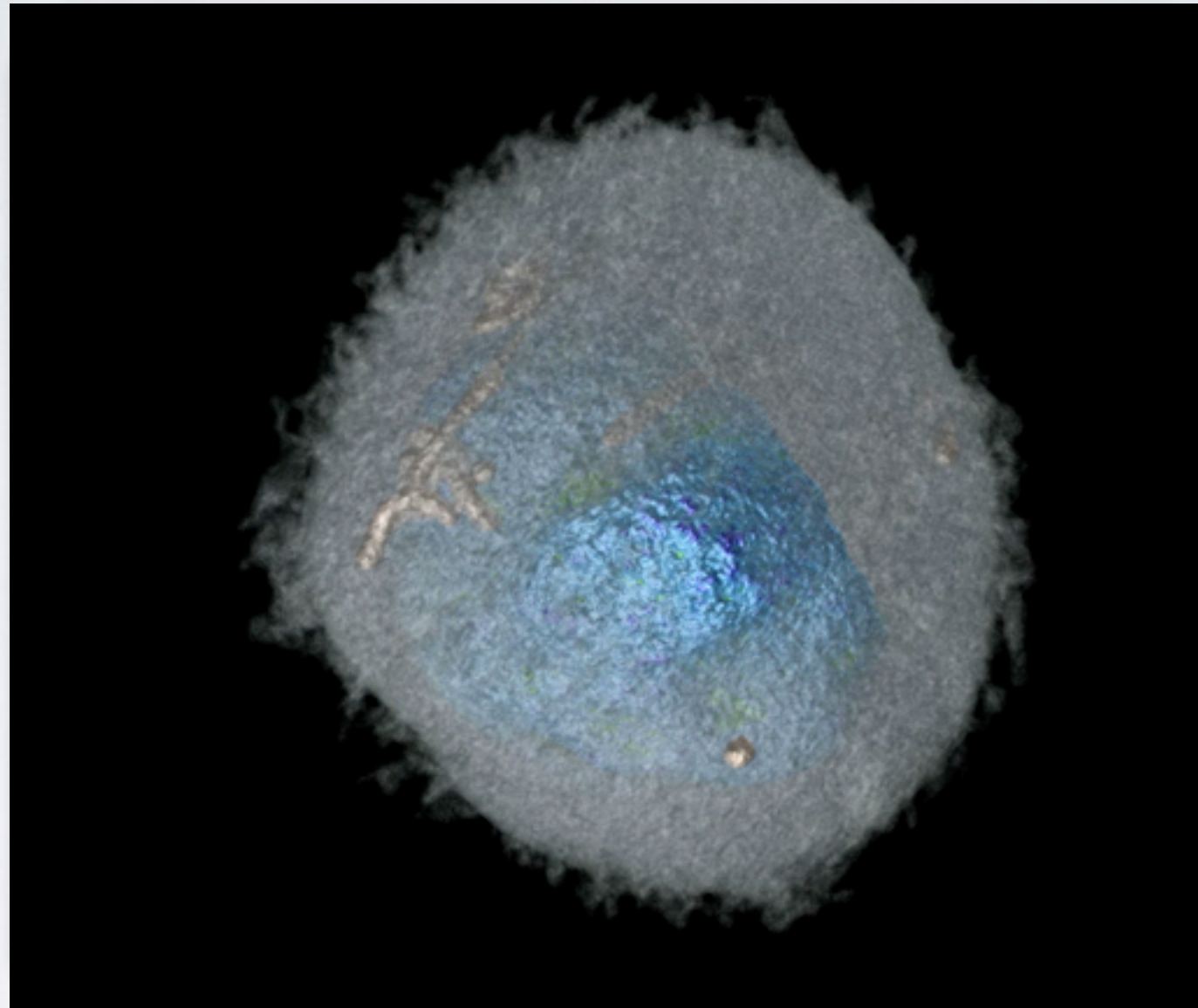
Alcohol oxidase
crystal in yeast cell

Calculated LAC $\Rightarrow 0.625 \mu\text{m}^{-1}$

Measured LAC $\Rightarrow 0.626 \mu\text{m}^{-1}$

SXT of human lymphoblastoid cell (Encode GM12878)

Volume rendered, segmented



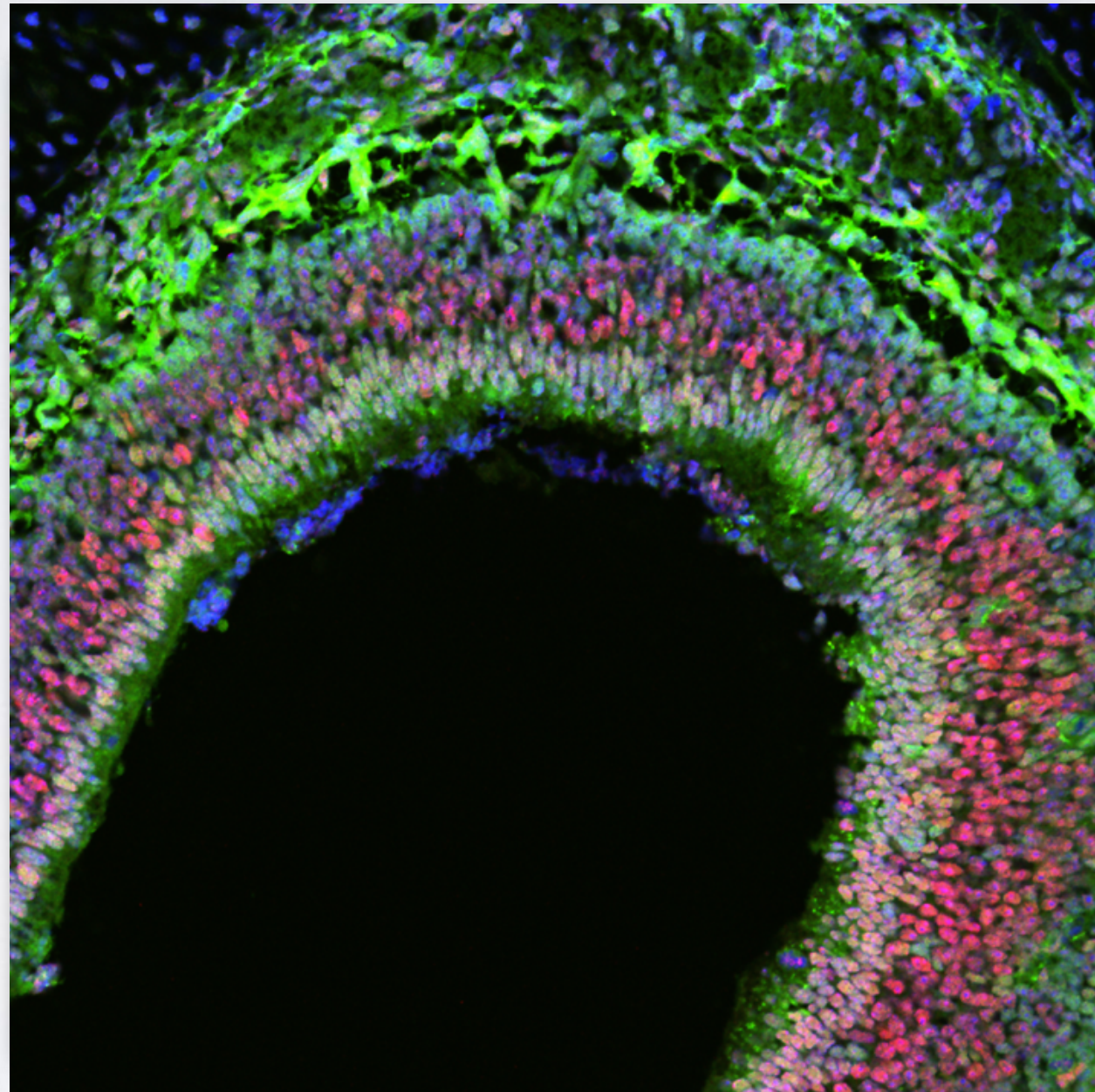
Cytoplasm - grey
Heterochromatin - blue
Euchromatin - green
Pericentromeric heterochromatin - gold
Mitochondria - bronze
Endoplasmic reticulum - red

Nuclear organization

Olfactory sensory neuron (OSN) differentiation

Mouse olfactory epithelium

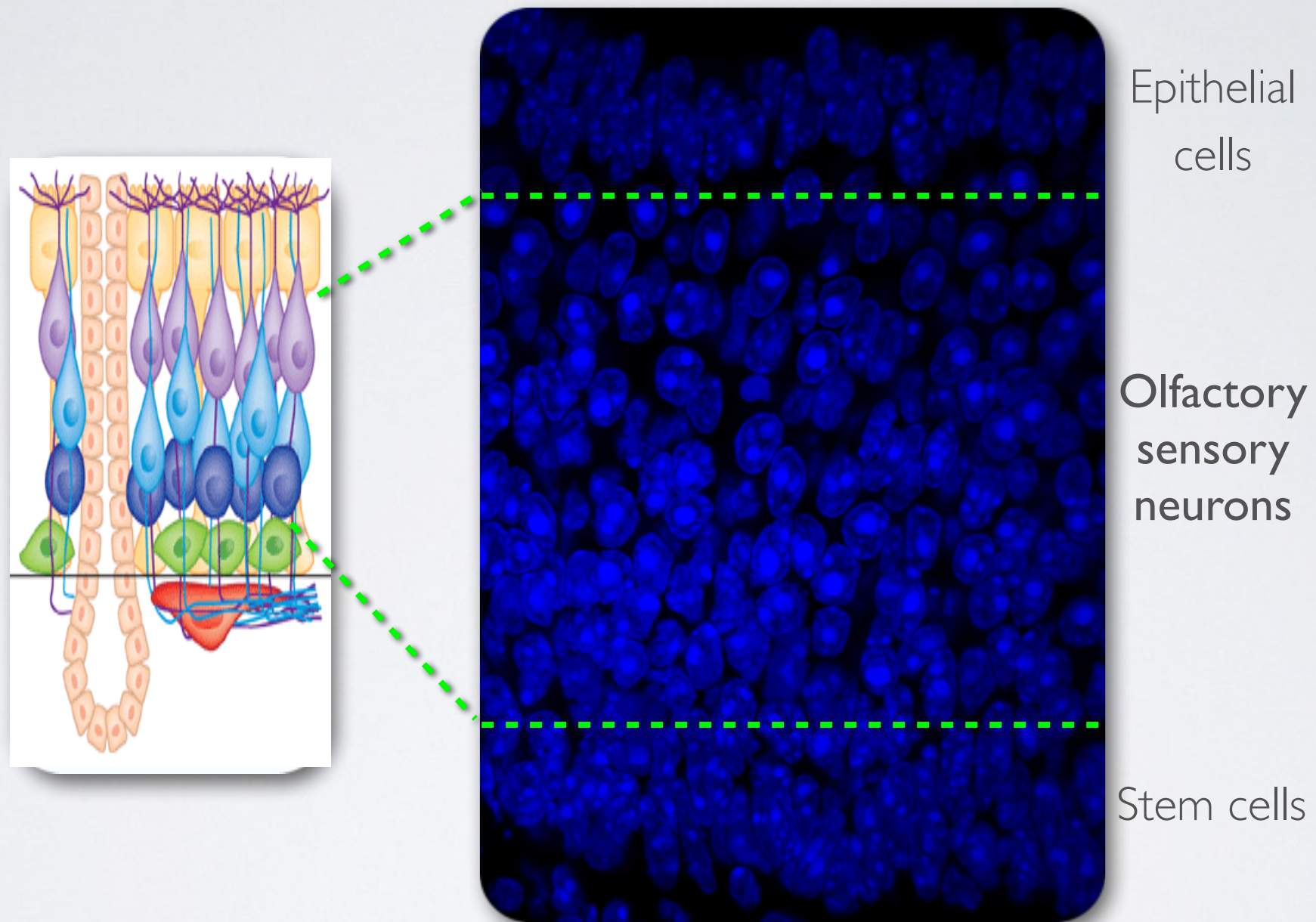
~ 1400 genes for olfaction in mice; each cell expresses just one



Stavros Lomvardas, UCSF

OR foci are silenced

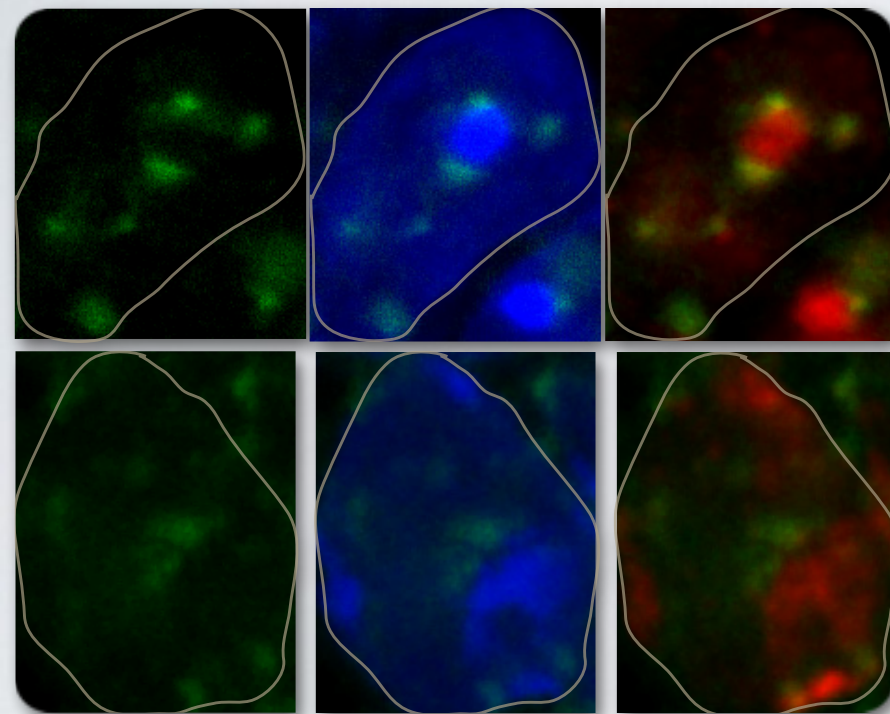
Heterochromatin in nucleus center



EJ Clowney, MA Le Gros, CP Mosley, FG Clowney, EC Markenskoff-Papadimitriou, M Myllys, G Barnea, CA Larabell and S Lomvardas. (2012) Cell 151, 724-737.

Structural organization critical for OR silencing

FISH

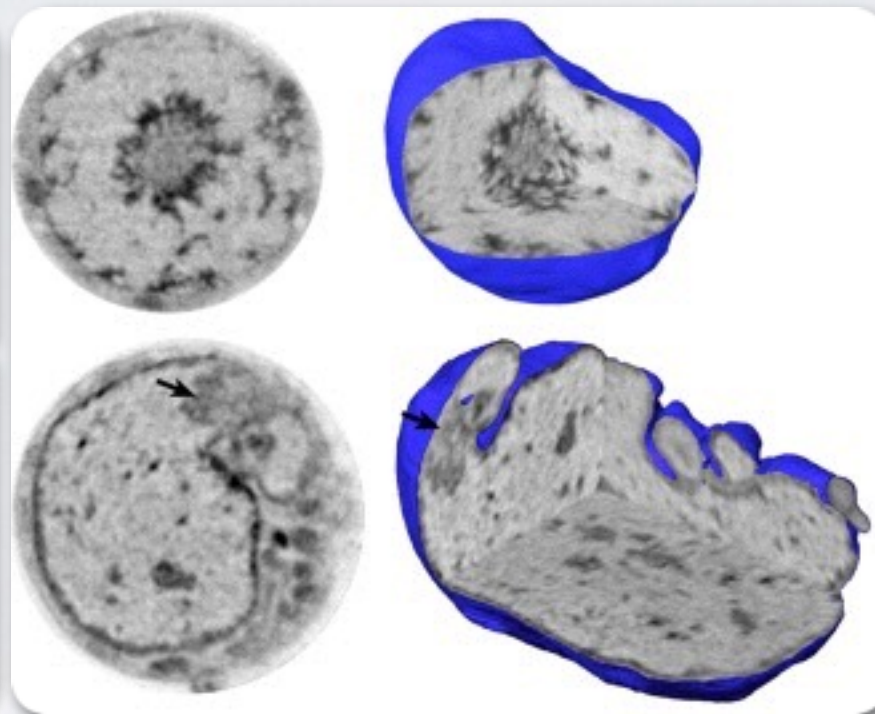


Pan OR

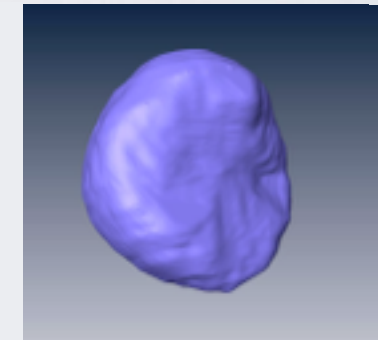
DAPI

HP1 β

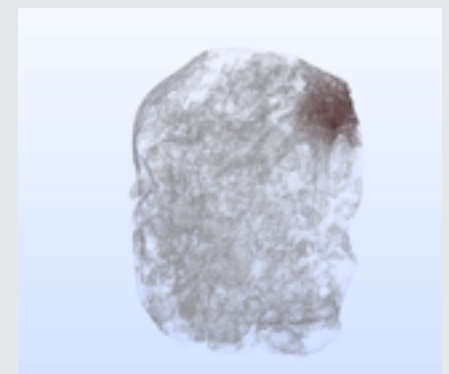
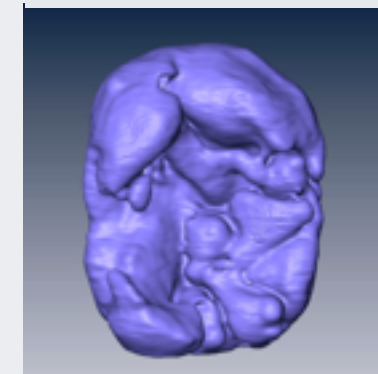
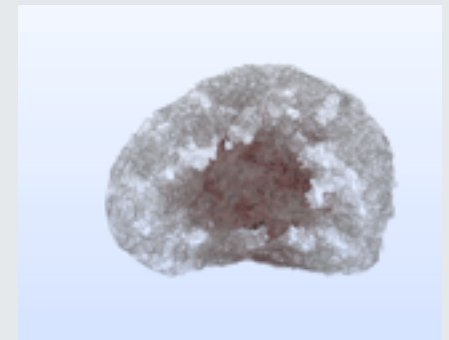
SXT orthoslices



SXT
surface
rendering



SXT
volume
rendering

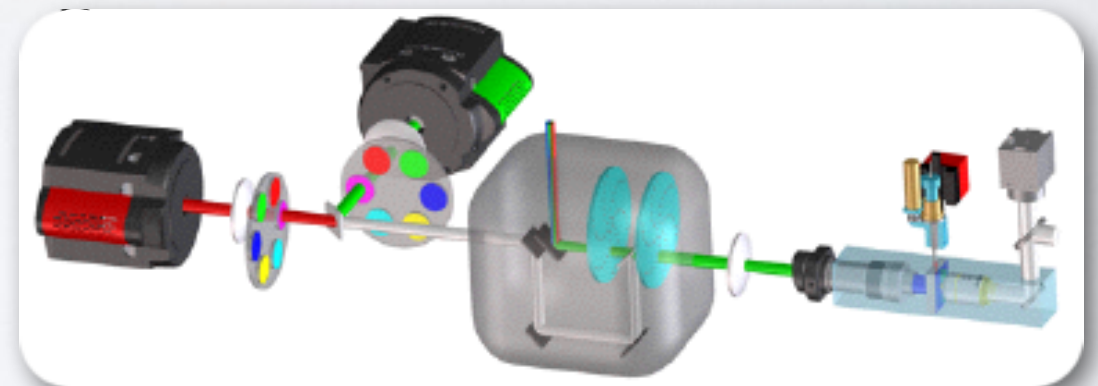
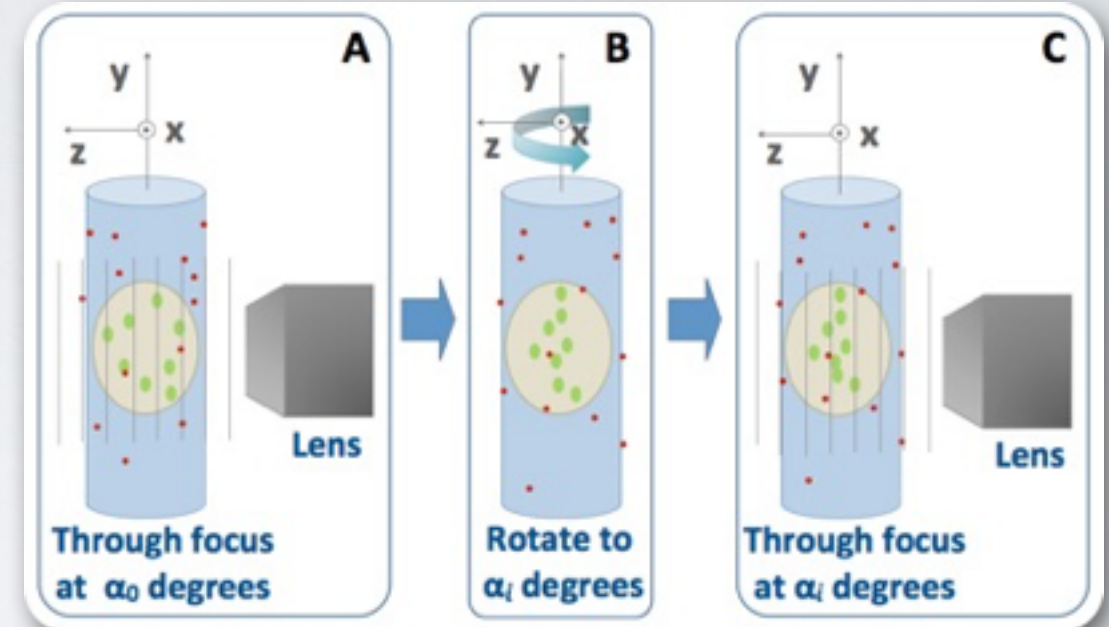
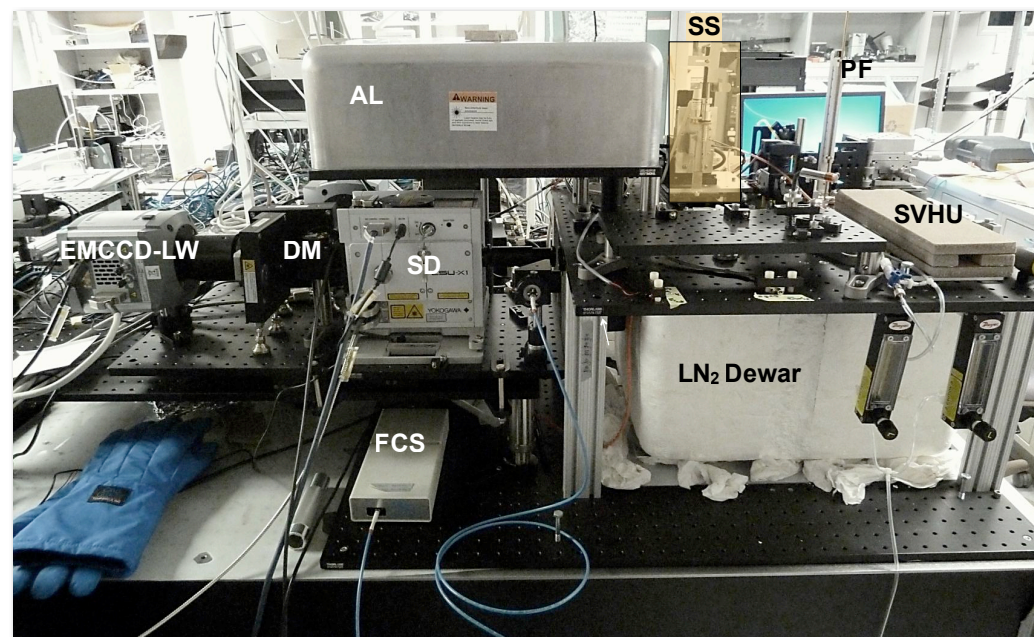
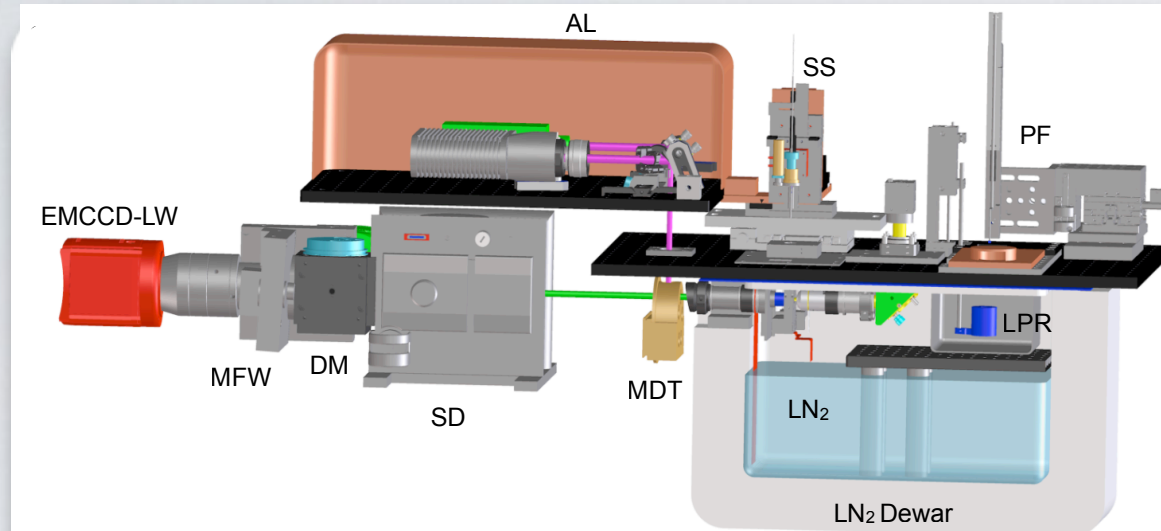


EJ Clowney, MA Le Gros, CP Mosley, FG Clowney, EC Markenskoff-Papadimitriou, M Myllys, G Barnea, CA Larabell and S Lomvardas. (2012) Cell 151, 724-737.

Unpublished data will be presented

Putting molecules in context

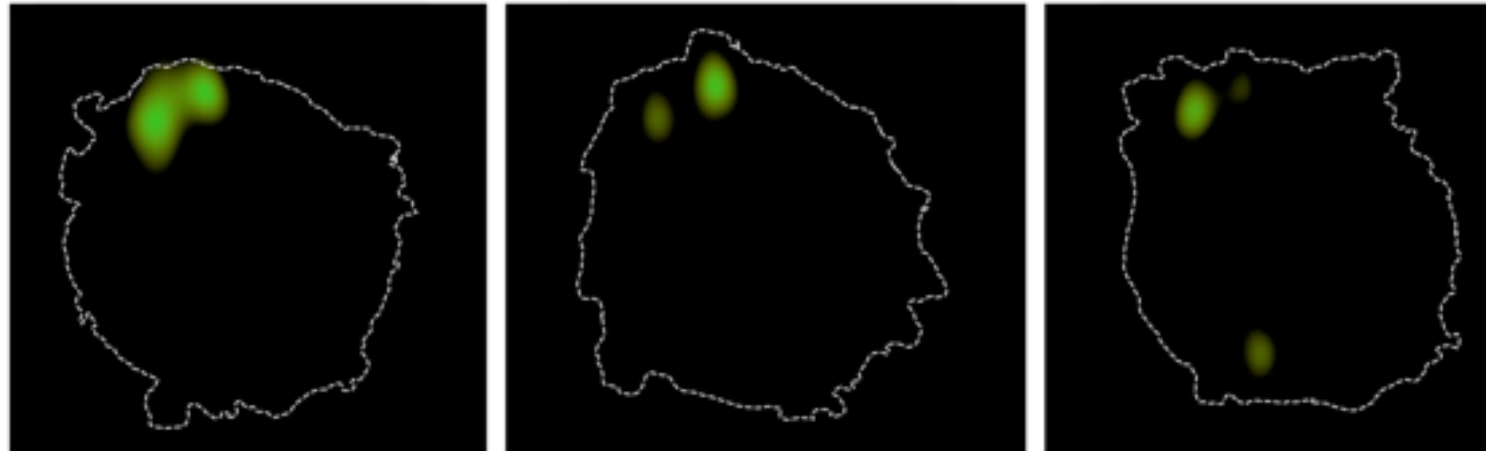
Cryo confocal tomography



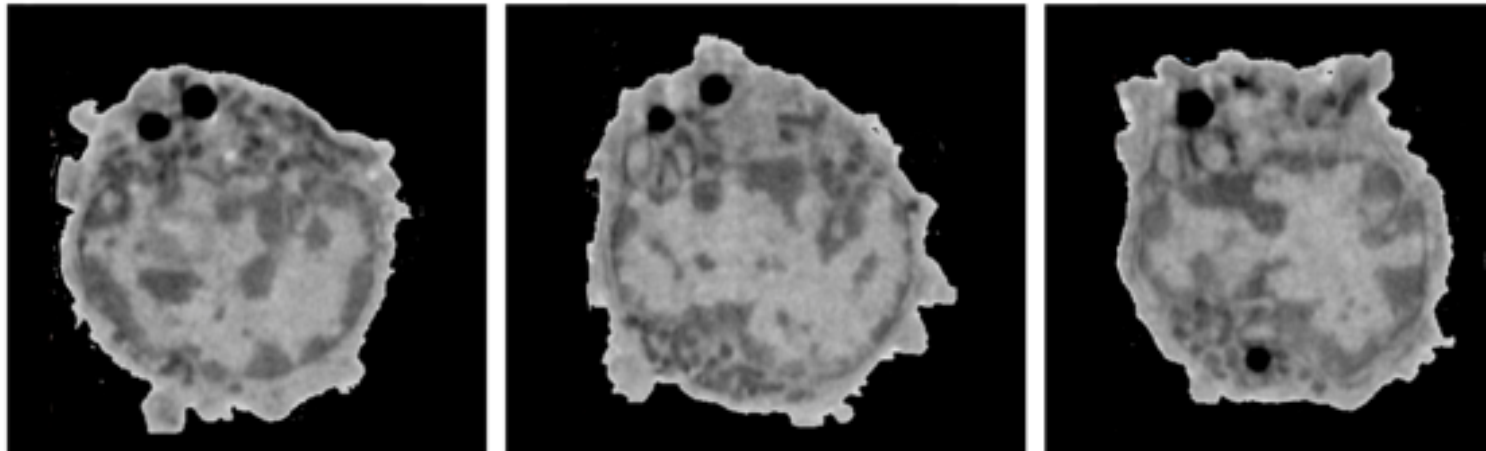
MA Le Gros et al. (2009). *J. Microscopy* 235(1):1-8

BODIPY labeled lipids in lymphoma cell

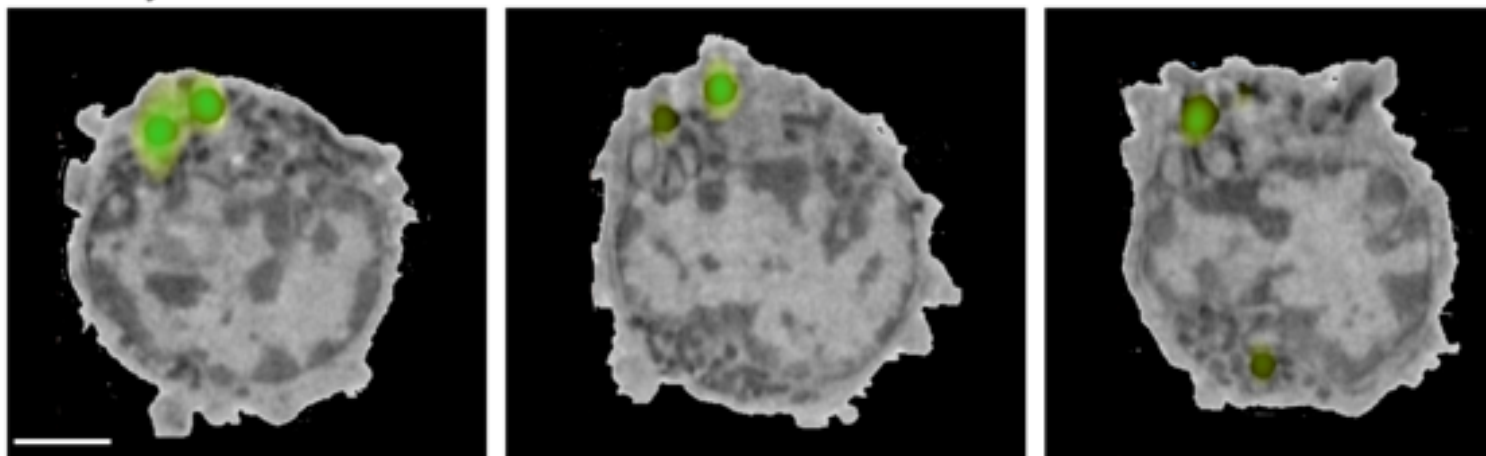
2D virtual slices from 3d cryogenic fluorescence tomography



2D virtual slices from the 3D soft x-ray tomographic reconstruction



Overlay of above fluorescence on SXT virtual sections



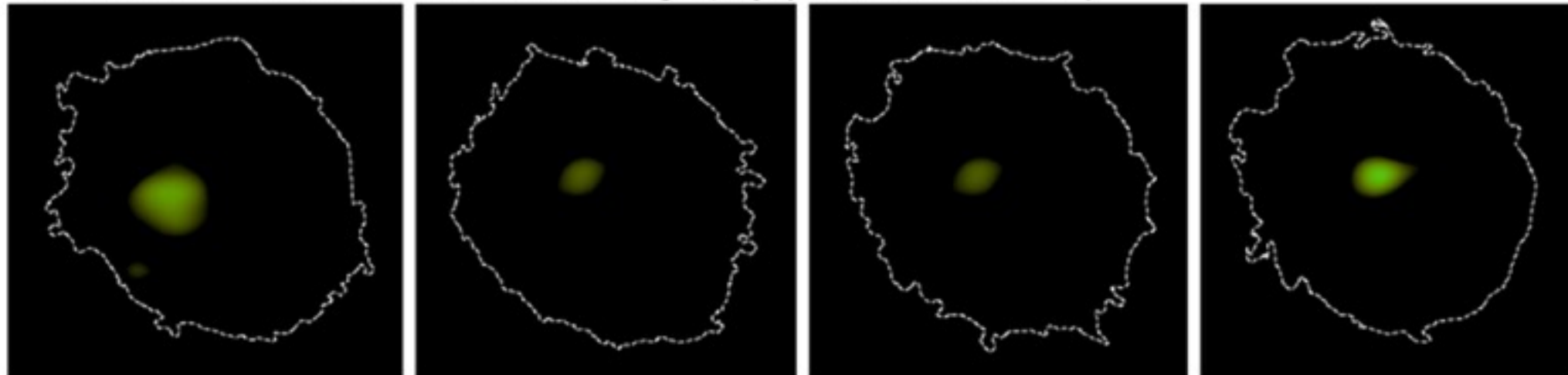
$z = 2.7 \mu\text{m}$

$z = 3.7 \mu\text{m}$

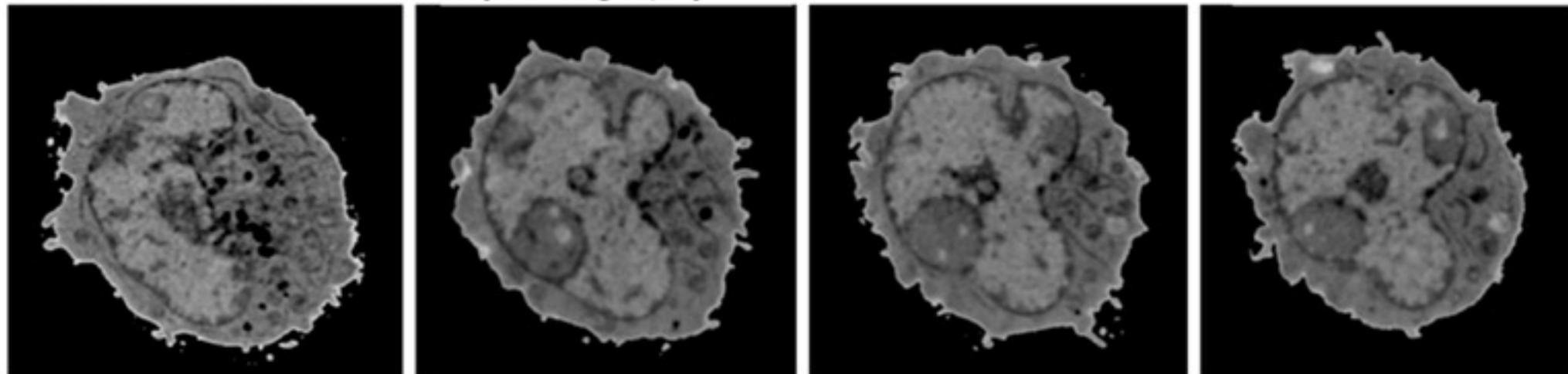
$z = 4.6 \mu\text{m}$

Inactive X chromosome

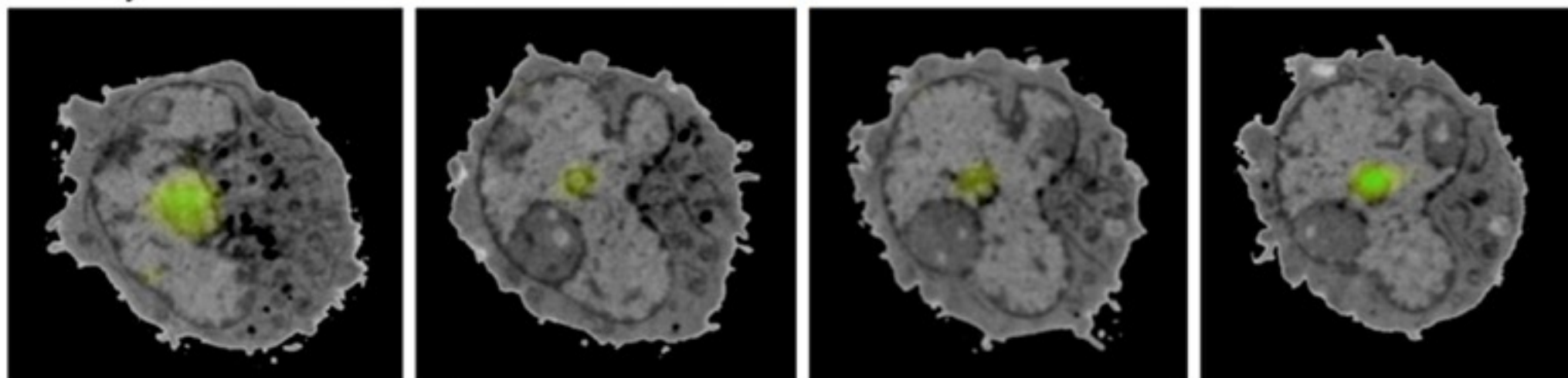
2D orthoslices from fluorescence tomography (MacroH2A-EGFP)



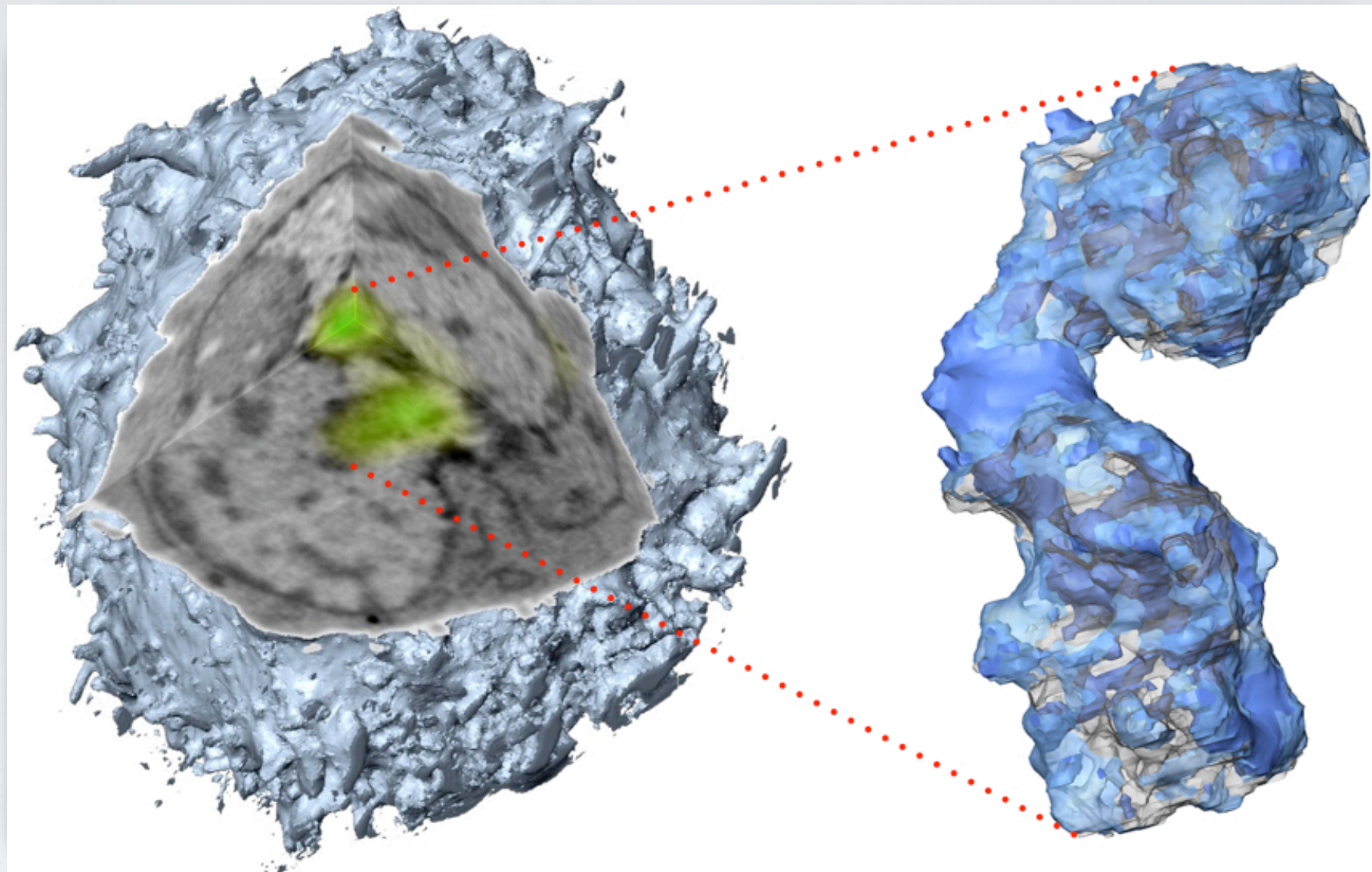
2D orthoslices from soft x-ray tomography



Overlay of above fluorescence on SXT orthoslices

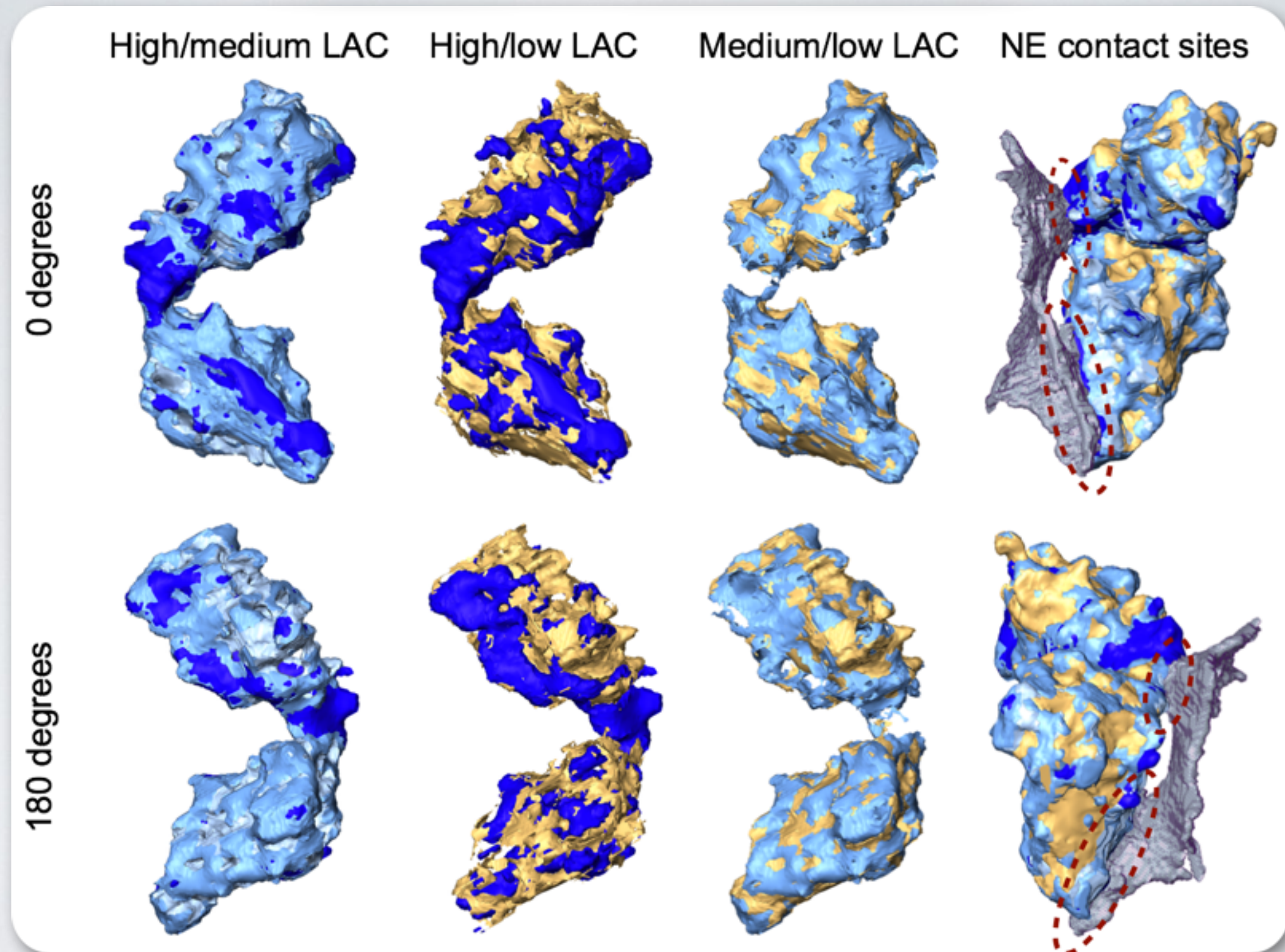


Inactive X chromosome

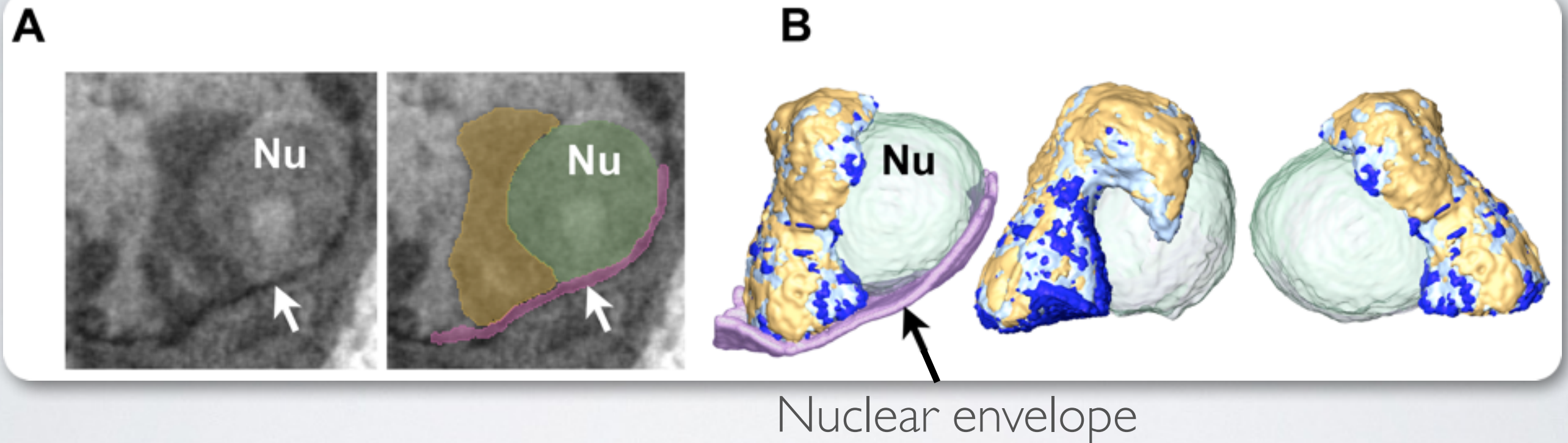


Smith EA, McDermott G, Do M, Leung K, Panning B, Le Gros MA and Larabell CA (2014). Quantitatively imaging chromosomes using correlated cryo-fluorescence and soft x-ray tomographies. *Biophysical Journal*. 107(8) 1988-96.

Inactive X chromosome



Inactive X chromosome



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